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OM protein - protein search, using sw model

Run on: December 3, 2002, 14:30:48 ; Search time 34 Seconds
(without alignments)
231.229 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 304
Sequence: 1 KVHSLARAGKVGQTGPKVA.....RRFVVVPTFGKKGNANS 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A.Geneseq_101002.*
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	304	100.0	59	15	AA198204
2	304	100.0	59	20	AA198381
3	304	100.0	66	23	AA198408
4	304	100.0	170	21	AA198439
5	276	90.8	118	22	AA198449
6	276	90.8	118	22	AA1984625
7	276	90.8	118	22	AA1985035
8	276	90.8	118	22	AA1985415
9	276	90.8	118	22	AA1986811
10	276	90.8	118	22	AA1986820

11	276	90.8	118	22	AA198618
12	276	90.8	118	22	AA1986364
13	276	90.8	118	22	AA1987354
14	263	86.5	132	22	AA1987093
15	239	78.6	62	21	AA1987253
16	239	78.6	62	21	AA1987888
17	239	78.6	62	21	AA1988419
18	239	78.6	62	21	AA1988832
19	239	78.6	83	21	AA1988882
20	239	78.6	84	21	AA1988887
21	239	78.6	93	21	AA1989118
22	239	78.6	110	21	AA1989886
23	239	78.6	130	21	AA1989728
24	238	78.3	62	21	AA1989704
25	238	78.3	62	21	AA1989788
26	238	78.3	82	21	AA1989703
27	238	78.3	130	21	AA1989569
28	231	76.0	62	21	AA1989311
29	231	76.0	62	21	AA1989348
30	231	76.0	62	21	AA1989861
31	231	76.0	62	21	AA1989476
32	231	76.0	62	21	AA1989690
33	231	76.0	68	21	AA1989871
34	211.5	69.6	312	22	AA1989872
35	211	69.4	157	22	AA1989565
36	208	68.4	41	17	AA1989681
37	208	68.4	108	22	AA1989728
38	208	68.4	108	22	AA19897519
39	201	66.1	40	22	AA1989731
40	188.5	62.0	58	21	AA1989318
41	175	57.6	61	22	AA19897230
42	175	57.6	90	22	AA19897520
43	168.5	55.4	129	22	AA19897113
44	163	53.6	35	22	AA19897113
45	123.5	40.6	459	23	AA19894132

ALIGNMENTS

RESULT 1
AA198204
ID AA198204 standard; protein; 59 AA.
XX
AC AA198204;
XX
DT 12-JUL-1994 (first entry)
XX
DE Heparin-binding protein.
XX
KW Cell growth agent; wound; bone disease; treatment; treating; agent.
XX
OS Rattus norvegicus.
XX
PN JP05339287-A.
XX
PD 21-DEC-1993.
XX
PF 05-JUN-1992; 92JP-0145125.
XX
PR 05-JUN-1992; 92JP-0145125.
XX
RA (FARH) HOECHST JAPAN LTD.
XX
DR WPI; 1994-031824/04.
XX
PT New heparin-binding protein - used as a cell growth agent for
XX treatment of wounds and bone disease
XX
PS Claim 1; Page 3; 4pp; Japanese.
XX
CC The sequence is that of a heparin binding-protein which is useful as
a cell growth agent and in the treatment of wounds and bone disease.

XX SQ Sequence 59 AA;
Query Match 100.0%; Score 304; DB 15; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.5e-32;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVHGLARAGKVRGOTPKVAKQEKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59
Db 1 KVHGLARAGKVRGOTPKVAKQEKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59

RESULT 2
AAW95381 ID AAW95381 standard; peptide; 59 AA.
XX AC AAW95381;
XX 17-MAR-1999 (first entry)
XX Antimicrobial peptide fragment from ubiquicidine.
XX Ubiquicidine; treatment; diagnosis; prophylaxis; infection; microbial;
XX pathogenic; Gram-positive bacteria; antimicrobial; Staphylococcus aureus;
XX Listeria monocytogenes; Gram-negative; Klebsiella pneumoniae; E. coli;
XX enterococcus; Salmonella typhimurium; Mycobacterium avium; M. fortuitum;
XX fungus; Candida albicans; Cryptococcus neoformans; Aspergillus fumigatus;
XX virus; parasite; Trypanosoma cruzi; Taxoplasma gondii.
XX Synthetic.
XX Mus sp.
XX WO9854314-A1.
XX 03-DEC-1998.
XX 29-MAY-1998; 98WO-NL00311.
XX 29-MAY-1997; 97NL-1006164.
XX (UYLE-) RIJKSUNIV LEIDEN.
XX Feitsma RIJ, Hiemstra PS, Nibbering PH, Pauwels EKJ;
XX Van Den Barselaar WT;
XX WPI; 1999-070214/06.
XX New antimicrobial peptides derived from ubiquicidine - useful for
XX the prophylaxis, diagnosis and treatment of infections in humans and
XX animals
XX Claim 2; Page 23; 48pp; English.
XX Sequences AAW95381-389 represent antimicrobial peptide fragments derived
XX from ubiquicidine. Ubiquicidine or optionally modified peptide fragments
XX of ubiquicidine, may be used for the treatment, diagnosis, or
XX prophylaxis of infections in humans and animals. In particular the
XX products and methods are directed against microbial infections caused by
XX pathogenic Gram-positive Staphylococcus aureus, including antibiotic
XX resistant strains, Listeria monocytogenes, and Gram-negative antibiotic
XX resistant Klebsiella pneumoniae, E. coli, enterococci, and Salmonella
XX typhimurium bacteria, micro-organisms difficult to treat such as
XX Mycobacterium avium and M. fortuitum, fungi such as Candida albicans,
XX Cryptococcus neoformans, and Aspergillus fumigatus, viruses, in
XX particular enveloped viruses, and parasites such as Trypanosoma cruzi and
XX Taxoplasma gondii.

XX SQ Sequence 59 AA;
Query Match 100.0%; Score 304; DB 20; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.5e-32;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVHGLARAGKVRGOTPKVAKQEKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59
Db 1 KVHGLARAGKVRGOTPKVAKQEKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNANS 59

RESULT 3
ABP42408 ID ABP42408 standard; Protein; 66 AA.
XX AC ABP42408;
XX 22-AUG-2002 (first entry)
XX Human ovarian antigen HOCWY79, SEQ ID NO:3540.
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
XX ovarian cancer; breast cancer; tumour; reproductive system disorder;
XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
XX PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
XX inflammatory condition; immune disorder; blood disorder;
XX cardiovascular disorder; respiratory disorder; neurological disorder;
XX gastrointestinal disorder; urinary system disorder; drug screening;
XX Gene therapy; chromosome mapping; forensic analysis;
XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;
XX antiinflammatory; gynaecological; reproductive.
XX Homo sapiens.
XX WO200200677-A1.
XX 03-JAN-2002.
XX 07-JUN-2001; 2001WO-US18569.
XX 07-JUN-2000; 2000US-209467P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Birse CE, Rosen CA;
XX WPI; 2002-147878/19.
XX N-PSDB; ABQ55485.
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g.
XX ovarian cancer), immune disorders, cardiovascular disorders and
XX neurological diseases -
XX Claim 11; SEQ ID NO 3540; 2922pp; English.
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigens, and the use
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX treating, prognosing or preventing various ovary and/or breast-related
XX disorders. Such conditions include ovarian cancer and breast cancer, and
XX metastatic tumours of ovarian or breast origin, reproductive system
XX disorders (e.g., infertility, disorders of pregnancy, anovulation,
XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis), and toxic
XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
XX vaginitis), immune disorders (e.g., congenital and acquired
XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
XX blood-related disorders (e.g., anaemia), cardiovascular disorders,
XX respiratory disorders, neurological disorders, gastrointestinal disorders
XX and urinary system disorders. Ovarian antigen polypeptides and
XX polynucleotides may also be used in screening for compounds which
XX modulate ovarian antigen expression or activity. The polynucleotides may
XX further be used for gene therapy, chromosome mapping, in the
XX identification of individuals and in forensic analysis, and the

CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 66 AA;

Query Match 100.0%; Score 304; DB 23; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.8e-32;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKHGSLARAGKVRGQTPKVAKEKKKKTKGRAKRRMQYRRFVNVVPTFGKKKGPANNS 59
DB 8 KKHGSLARAGKVRGQTPKVAKEKKKKTKGRAKRRMQYRRFVNVVPTFGKKKGPANNS 66

RESULT 4
AAB43549
ID AAB43549 standard; Protein; 170 AA.

XX AAB43549;
DT 08-FEB-2001 (first entry)

DE Human cancer associated protein sequence SEQ ID NO:994.

XX Human; cancer associated gene; cancer antigen; detection; cancer;
KM diagnosis; cytostatic; proliferative; vunerary; immunomodulator;
KM antidiabetic; antiaesthetic; antirheumatic; antiarthritic; antiviral;
KM antiinflammatory; antihypertoid; antiallergic; antibacterial; cardiac;
KM dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KM vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KM immune disorder; haematopoietic cell disorder; autoimmune disorder;
KM allergic reaction; graft versus host disease; organ rejection;
KM haemostatic; thrombolytic; cardiovascular disorder; infection;
KM neurological disease; drug screening.

XX Homo sapiens.

PN WO200055350-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US05882.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

XX WPI; 2000-587533/55.

DR N-PSDB; AAC77758.

XX Novel isolated nucleic acids comprising sequences encoding peptides
PT useful for treating or diagnosing e.g. cancer -

PS Claim 11; Page 1568-1569; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given
CC in AAB43398 to AAB44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vunerary; immunomodulator;
CC antidiabetic; antiaesthetic; antirheumatic; antiarthritic;
CC antiinflammatory; antihypertoid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;
CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating

CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB44240 represent sequences used in the exemplification of
CC the present invention.

XX Sequence 170 AA;

Query Match 100.0%; Score 304; DB 21; Length 170;
Best Local Similarity 100.0%; Pred. No. 8.1e-33;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKHGSLARAGKVRGQTPKVAKEKKKKTKGRAKRRMQYRRFVNVVPTFGKKKGPANNS 59
DB 112 KKHGSLARAGKVRGQTPKVAKEKKKKTKGRAKRRMQYRRFVNVVPTFGKKKGPANNS 170

RESULT 5
AAB29449
ID AAB29449 standard; Peptide; 118 AA.

XX AAB29449;

DT 01-FEB-2002 (first entry)

DE Peptide #2100 encoded by breast cell single exon nucleic acid probe.

XX Human; microarray; single exon probe; gene expression; breast;
KM disease; cancer.

XX Homo sapiens.

PN WO200157271-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00662.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 23-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-496933/54.

DR 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -

PS Claim 27; SEQ ID NO 12417; 327pp + sequence listing; English.

XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater

Matches	56;	Conservative	1;	Mismatches	2;	Indels	4;	Gaps	1;
Qy	1	KVHGSILARAGKRGCTPPKAAKOEK----	KKTTGRAKRMQYNRRFVNVPVTFGKKKGGN	56					
Db	56	KVHGSILARAGKRGCTPPKAAKOEKKKKKKKKKTGATRRMQYNRRFVNVPVTFGKKKGGN	115						
Qy	57	ANS 59							
Db	116	ANS 118							
RESULT 8									
ID	AAM55415	AAM55415 standard; Protein; 118 AA.							
AC	AAM55415;								
DT	05-NOV-2001	(first entry)							
DE	Human brain expressed single exon probe encoded protein SEQ ID NO: 27520.								
XX	Human; brain expressed exon; gene expression analysis; probe;								
KW	miccoarray; Alzheimer's disease; multiple sclerosis; schizophrenia;								
KW	epilepsy; cancer.								
XX	Homo sapiens.								
OS	WO200157275-A2.								
PN	09-AUG-2001.								
PD	30-JAN-2001; 2001WO-US00667.								
PF	04-FEB-2000; 2000US-0180312.								
PR	26-MAY-2000; 2000US-0207456.								
PR	30-JUN-2000; 2000US-0608408.								
PR	03-AUG-2000; 2000US-0632366.								
PR	21-SEP-2000; 2000US-0234687.								
PR	27-SEP-2000; 2000US-0236359.								
PR	04-OCT-2000; 2000GB-0024263.								
XX	(MOLE-) MOLECULAR DYNAMICS INC.								
PA	Penn SG, Hanzel DK, Chen W, Rank DR;								
PI	WPI; 2001-483446/52.								
XX	Single exon nucleic acid probes for analyzing gene expression in human								
PT	brains -								
PS	Example 4; SEQ ID NO: 27520; 650bp + Sequence Listing; English.								
XX	The present invention provides a number of single exon nucleic acid								
CC	probes which are derived from genomic sequences expressed in the human								
CC	brain. They can be used to measure gene expression in brain cell samples,								
CC	which may enable the diagnosis and improved treatment of nervous system								
CC	diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,								
CC	epilepsy and cancers. The present sequence is a protein encoded by one of								
CC	the probes of the invention.								
XX	Sequence 118 AA;								
XX	Query Match 90.8%; Score 276; DB 22; Length 118;								
XX	Best Local Similarity 88.9%; Pred. No. 2.5e-28;								
XX	Matches 56; Conservative 1; Mismatches 2; Indels 4; Gaps 1								
Qy	1	KVHGSILARAGKRGCTPPKAAKOEK----	KKTTGRAKRMQYNRRFVNVPVTFGKKKGGN	56					
Db	56	KVHGSILARAGKRGCTPPKAAKOEKKKKKKKKKTGATRRMQYNRRFVNVPVTFGKKKGGN	115						
Qy	57	ANS 59							
Db	116	ANS 118							

RESULT 9
AAM67811
ID AAM67811 standard; Protein: 118 AA.
XX
AC AAM67811;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28117.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS Homo sapiens.
PN WO200157276-A2.
PD
XX 09-AUG-2001.
PX
PF 30-JAN-2001; 2001WO-US00668.
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
PS Example 4; SEQ ID NO: 28117; 658bp + Sequence Listing; English.
CC The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
SC Sequence 118 AA;
Query Match 90.8%; Score 276; DB 22; Length 118; Best Local Similarity 88.9%; Pred. No. 2,5e-28; Matches 56; Conservative 1; Mismatches 2; Indels 4; Gaps 1;
OY 1 KYHGLABAGKVGROTPYAKOEKK-----KKKTGRAKRMQYRRFRVVNVPFGKKKGP 56 DB 56 KYHGLABAGKVGROTPYAKOEKKKKRKKTKGTATRMQINRRFVNVPFFSKKKGPN 115
OY 57 ANS 59 DB 116 ANS 118
RESULT 10
AAM15620
ID AAM15620 standard; Protein: 118 AA.
XX
AC AAM15620;
XX
DT 12-OCT-2001 (first entry)
XX
PE Peptide #2054 encoded by probe for measuring cervical gene expression.

```
XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX KW cervical cancer.
XX OS Homo sapiens.
XX PN WO200157278-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00663.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PS WPI; 2001-488901/53.
XX DR
XX XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX PS Claim 27; SEQ ID No 20446; 487pp; English.
XX CC The present invention relates to human single exon nucleic acid probes
CC (SENP: see Aa110068-AA128459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX XX
XX SQ Sequence 118 AA;
Query Match 90.8%; Score 276; DB 22; Length 118;
Best Local Similarity 88.9%; Pred. No. 2.5e-28;
Matches 56; Conservative 1; Mismatches 2; Indels 4; Gaps 1;
Qy 1 KVHGLARAGKVRGQTPKVAQEKK----KKKTGRAKRMQYNRRFVNVPVTFGKKKGP 56
Db 56 KVHGLARAGKVRGQTPKVAQEKKKKKKKKKTQATRRMQYNRRFVNVPVTFGKKKGP 115
Qy 57 ANS 59
Db 116 ANS 118
RESULT 11
AAM28118
ID AAM28118 standard; Protein; 118 AA.
XX AC AAM28118;
XX DT 17-OCT-2001 (first entry)
XX DE Peptide #2155 encoded by probe for measuring placental gene expression.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.
XX OS Homo sapiens.
XX XX
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PN WO200157272-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00663.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PS WPI; 2001-488897/53.
XX DR
XX XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX PS Claim 27; SEQ ID No 28387; 654pp; English.
XX CC The present invention relates to single exon nucleic acid probes (SENP:
CC see Aa131315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX XX
XX SQ Sequence 118 AA;
Query Match 90.8%; Score 276; DB 22; Length 118;
Best Local Similarity 88.9%; Pred. No. 2.5e-28;
Matches 56; Conservative 1; Mismatches 2; Indels 4; Gaps 1;
Qy 1 KVHGLARAGKVRGQTPKVAQEKK----KKKTGRAKRMQYNRRFVNVPVTFGKKKGP 56
Db 56 KVHGLARAGKVRGQTPKVAQEKKKKKKKKKTQATRRMQYNRRFVNVPVTFGKKKGP 115
Qy 57 ANS 59
Db 116 ANS 118
RESULT 12
AAM03364
ID AAM03364 standard; Protein; 118 AA.
XX AC AAM03364;
XX DT 09-OCT-2001 (first entry)
XX DE Peptide #2046 encoded by probe for measuring breast gene expression.
XX KW Probe; human; breast disease; breast cancer; development disorder;
XX KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX OS Homo sapiens.
XX PN WO200157270-A2.
XX PD 09-AUG-2001.
XX PF 29-JAN-2001; 2001WO-US00661.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
```

PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
XX
XX Novel single exon nucleic acid probe used to measuring gene expression
PT in a human breast -
XX
PS Claim 27; SEQ ID No 12104; 322pp; English.
XX
XX The present invention relates to novel single exon nucleic acid probes
CC (see A100010-A110067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridizes at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic
CC aetiology. The diseases include: breast cancer, disorders of development,
CC inflammatory diseases of the breast, fibrocystic changes, proliferative
CC breast disease and non-carcinoma tumours.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 118 AA:

Query Match 90.8%; Score 276; DB 22; Length 118;
Best Local Similarity 88.9%; Pred. No. 2.5e-28;
Matches 56; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 1 KVGSLARAGKVGQTPKVAKEKK---KKKTGRAKRMQVNRFRVNVPTFGKKKGN 56
DB 56 KVGSLARAGKVGQTPKVAKEKKKKKKKTGTATRMQVNRFRVNVPTFGKKKGN 115

QY 57 ANS 59
DB 116 ANS 118

RESULT 13
ABG37354
ID ABG37354 standard; Peptide; 118 AA.
XX
AC ABG37354;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 27019.
XX
XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Heremansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
XX Homo sapiens.
OS
XX WO200186003-A2.
PN
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US00665.
XX
XX 04-FEB-2000; 2000US-180312P.
PR 26-MAY-2000; 2000US-207456P.
PR

PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX
PS Claim 27; SEQ ID No 27019; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of
CC probes; the novel set of probes which hybridise at high stringency to a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung; comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarray having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Heremansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
CC pulmonary alveolar proteinosis, Karsenger syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a peptide/protein
CC encoded by a single exon probe of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 118 AA:

Query Match 90.8%; Score 276; DB 23; Length 118;
Best Local Similarity 88.9%; Pred. No. 2.5e-28;
Matches 56; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 1 KVGSLARAGKVGQTPKVAKEKK---KKKTGRAKRMQVNRFRVNVPTFGKKKGN 56
DB 56 KVGSLARAGKVGQTPKVAKEKKKKKKKTGTATRMQVNRFRVNVPTFGKKKGN 115

QY 57 ANS 59
DB 116 ANS 118

RESULT 15
AAG22753
ID AAG22753 standard; Protein; 62 AA.
XX
AC AAG22753;
XX
DT 17-OCT-2000 (first entry)
XX
XX
DE Zea mays protein fragment SEQ ID NO: 25803.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.


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PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0143390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 09-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.

PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158293.
PR 13-OCT-1999; 99US-0158294.
PR 13-OCT-1999; 99US-0158295.
PR 14-OCT-1999; 99US-0158329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161921.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 78.6%; Score 239; DB 21; Length 62;
Best Local Similarity 79.3%; Pred. No. 8,4e-24;
Matches 46; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KKHGSLARAGKRGOTPPKAKOEKKKKKTGRARRMQYNNRFPVNVPTFGKKKPNAN 58
Db 3 KKHGSLARAGKRGOTPPKAKODKKKKPRGRARRMQYNNRFPVTVVGFKKRPNSS 60

Search completed: December 3, 2002, 14:31:59
Job time : 36 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 3, 2002, 14:30:48 ; Search time 20 seconds
(without alignments)
283.597 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 304

Sequence: 1 KVHGSLLARAGKVRGQTPKVA.....RRFNVVPTFGKKKGNANS 59

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries.

Database :

1: PIR_73:*
2: pir1:*
3: pir2:*
4: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	304	100.0	133	1 A47416	ubiquitin-like pro
2	304	100.0	133	2 JCI278	ubiquitin-like pro
3	304	100.0	133	2 T48346	ribosomal protein
4	231	76.0	62	2 H85342	RIBOSOMAL PROTEIN
5	231	76.0	68	2 F84580	40S ribosomal prot
6	227	74.7	130	2 T15642	hypothetical prote
7	188.5	62.0	58	2 A71604	ribosomal protein
8	176	57.9	61	2 T39834	ribosomal protein
9	175.5	57.7	63	1 S67074	ribosomal protein
10	107	35.2	229	2 S36383	ribosomal protein
11	104.5	34.4	52	2 G90244	SEB4B protein - hu
12	91.5	30.1	50	2 C72528	15U ribosomal prot
13	66	21.7	212	2 S73991	probable ribosomal
14	64.5	21.2	454	1 A45340	ribosomal protein
15	64.5	21.2	454	1 B45340	nucleocapsid prote
16	64.5	21.2	454	1 C45340	nucleocapsid prote
17	64.5	21.2	454	1 A45396	nucleocapsid prote
18	64.5	21.2	455	1 VHIHMJ	nucleocapsid prote
19	64.5	21.2	455	1 D45340	nucleocapsid prote
20	64	21.1	225	2 AC1896	nucleocapsid prote
21	63.5	20.9	1526	2 A45605	hypothetical prote
22	63	20.6	207	2 JCI129	mature-parasite-in
23	62.5	20.6	207	2 JCI129	hypothetical prote
24	62.5	20.6	207	2 JCI129	hypothetical prote
25	60.5	19.9	186	2 B61611	high-mobility grou
26	60.5	19.9	617	2 S27389	nonhistone chromos
27	60	19.7	439	2 JQ1729	secretogranin II -
28	60	19.7	521	2 T37504	ankyrin-repeat pro
29	59.5	19.6	205	2 S34919	hypothetical prote
					ribosomal protein

30	59.5	19.6	752	2 S64750	probable ATP-depen
31	59	19.4	133	2 H87589	EF hand domain pro
32	59	19.4	304	2 S44801	PI0E9.2 protein -
33	58	19.1	186	2 S30221	nonhistone chromos
34	58	19.1	209	1 NSHUR2	nonhistone chromos
35	58	19.1	210	2 A34719	nonhistone chromos
36	58	19.1	377	2 G84857	hypothetical prote
37	58	19.1	774	2 A24057	glycophorin-bindin
38	58	19.1	894	2 T15769	hypothetical prote
39	57.5	18.9	211	2 H64216	ribosomal protein
40	57.5	18.9	340	2 T33559	probable transposa
41	57.5	18.9	340	2 A80096	transposase for in
42	57.5	18.9	340	2 A80198	transposase for in
43	57.5	18.9	340	2 A80395	transposase for in
44	57.5	18.9	340	2 A80488	transposase for in
45	57.5	18.9	340	2 AC0031	transposase for in

ALIGNMENTS

RESULT 1

A47416
N/Contains: ribosomal protein S30; ubiquitin-like protein
C/Species: Rattus norvegicus (Norway rat)
C/Date: 21-Jul-2000 #sequence revision 21-Jul-2000 #text_change 21-Jul-2000
C/Accession: A47416; B47416; S18101
R/Olivera, J.; Wool, I.G.
J. Biol. Chem. 268, 17967-17974, 1993
A/Title: The carboxyl extension of a ubiquitin-like protein is rat ribosomal protein S30.
A/Reference number: A47416; MUID:93352612; PMID:8394356
A/Accession: A47416
A/Molecule type: mRNA
A/Residues: 1-133 <OLV>
A/Cross-References: EMBL:X62671; NID:9407165; PIDN:CAA44545.1; PID:957566
A/Accession: B47416
A/Molecule type: protein
A/Residues: 75-92 <OLV>
A/Note: The proteins are designated as ubiquitin-like protein and ribosomal protein S30
C/Superfamily: ubiquitin-like protein / rat ribosomal protein S30; ubiquitin homology
C/Keywords: protein biosynthesis; ribosome
F.1-74/Product: ubiquitin-like protein #status predicted <UBI>
F.1-74/Domains: ubiquitin homology <UBH>
F.75-133/Product: ribosomal protein S30 #status experimental <RIB>

Query Match 100.0%; Score 304; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.8e-25;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSLLARAGKVRGQTPKVAKEKKKTGAKRRMQRVNVVPTFGKKGNANS 59
DB 75 KVHGSLLARAGKVRGQTPKVAKEKKKTGAKRRMQRVNVVPTFGKKGNANS 133

RESULT 2
JCI278
ubiquitin-like protein / ribosomal protein S30, cytosolic - human
N/Alternate names: fau protein
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 24-Sep-1999
R/Kae, K.; Michiels, L.; Merregaert, J.
Biochem. Biophys. Res. Commun. 187, 927-933, 1992
A/Title: Genomic structure and expression of the human fau gene: Encoding the ribosomal
A/Reference number: JCI278; MUID:92412144; PMID:1326960
A/Accession: JCI278
A/Molecule type: DNA
A/Residues: 1-133 <KAS>
A/Cross-References: EMBL:X65921; NID:931304; PIDN:CAA46714.1; PID:931305
R/Michiels, L.; Van der Raaijlaert, E.; Van Hasselt, F.; Kae, K.; Merregaert, J.
Oncogene 8, 2537-2546, 1993
A/Title: fau cDNA encodes a ubiquitin-like-S30 fusion protein and is expressed as an anti

A:Reference number: I37387; MUID:93368957; PMID:8395683
A:Accession: I37387
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-133 <RES>
A:Cross-references: EMBL:X65923; NID:G31302; PIDN:CAA46716.1; PID:G31303
R:Vladimirov, S.N.; Ivanov, A.V.; Karpova, G.G.; Musolyamov, A.K.; Egorov, T.A.; Thiede, Eur. J. Biochem. 239, 144-149, 1996
A:Title: Characterization of the human small-ribosomal-subunit proteins by N-terminal an
A:Reference number: S68911; MUID:96305378; PMID:8706699
A:Accession: S68911
A:Molecule type: protein
A:Residues: 75-99 <VLA>
C:Genetics:
A:Gene: fau
A:Introns: 25/3; 74/1; 92/3
C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology
C:Keywords: protein biosynthesis; ribosome
F:1-74/Domain: ubiquitin homology <UBH>
F:75-133/Product: ribosomal protein S30, cytosolic #status experimental <MAT>

Query Match 100.0%; Score 304; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.8e-25;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVHGLARAGKVRGQTPKVAQKQKKKTGAKRRMQYNRRFVNVVPTFGKKKGPNNAS 59
Db 75 KVHGLARAGKVRGQTPKVAQKQKKKTGAKRRMQYNRRFVNVVPTFGKKKGPNNAS 133

RESULT 3
148346
ribosomal protein fau - mouse
N:Alternate names: gene fau protein; monoclonal nonspecific suppressor factor beta
C:Species: Mus musculus (house mouse)
C:Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text_change 24-Sep-1999
R:Accession: I48346; AS6532; I59368; S21452
R:Michaels, L.; Van der Raaij-Wel, E.; Van Hasselt, F.; Kas, K.; Merregaert, J.
Oncogene 8, 2537-2546, 1993
A:Title: fau cDNA encodes a ubiquitin-like-S30 fusion protein and is expressed as an an
A:Reference number: I37387; MUID:93368957; PMID:8395683
A:Accession: I48346
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-133 <RES>
A:Cross-references: EMBL:X65922; NID:G50949; PIDN:CAA46715.1; PID:G50950
R:Castells, D.; Poirier, C.; Guenet, J.L.; Merregaert, J.
Genomics 25, 291-294, 1995
A:Title: The mouse Fau gene: genomic structure, chromosomal localization, and characteri
A:Reference number: AS6532; MUID:95293388; PMID:7774934
A:Accession: AS6532
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <CAS>
A:Cross-references: GB:I33715; NID:G497610; PIDN:AAA91564.1; PID:G497611
A:Note: authors translated the codon GTT for residue 119 as Arg, and GTC for residue 120
R:Nakamura, M.; Xavier, R.M.; Tsunematsu, T.; Tanigawa, Y.
Proc. Natl. Acad. Sci. U.S.A. 92, 3463-3467, 1995
A:Title: Molecular cloning and characterization of a cDNA encoding monoclonal nonspecifi
A:Reference number: I59368; MUID:95241522; PMID:7724584
A:Accession: I59368
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-133 <RE2>
A:Cross-references: GB:D26610; NID:G1060926; PIDN:BAA05655.1; PID:G1060927
C:Genetics:
A:Gene: fau
A:Introns: 25/3; 74/1; 92/3
C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology
F:1-74/Domain: ubiquitin homology <UBH>

Query Match 100.0%; Score 304; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.8e-25;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVHGLARAGKVRGQTPKVAQKQKKKTGAKRRMQYNRRFVNVVPTFGKKKGPNNAS 59
Db 75 KVHGLARAGKVRGQTPKVAQKQKKKTGAKRRMQYNRRFVNVVPTFGKKKGPNNAS 133

RESULT 4
H85342
RIBOSOMAL PROTEIN S30 homolog [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: H85342
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spr
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: H85342
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <STO>
A:Cross-references: GB:NC_001268; NID:G7269837; PIDN:CAB79697.1; GSPDB:GN00140
C:Genetics:
A:Gene: At4g29390
A:Map position: 4

Query Match 76.0%; Score 231; DB 2; Length 62;
Best Local Similarity 75.9%; Pred. No. 8e-18;
Matches 44; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KVHGLARAGKVRGQTPKVAQKQKKKTGAKRRMQYNRRFVNVVPTFGKKKGPNNAN 58
Db 3 KVHGLARAGKVRGQTPKVAQKQKKKPRGAHKRLQHNRRFVTAVVVGFGKKRGPNS 60

RESULT 5
F84580
40S ribosomal protein S30 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
C:Accession: F84580
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, I.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84580
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-68 <STO>
A:Cross-references: GB:AE002093; NID:G3687243; PIDN:AAC62141.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g19750
A:Map position: 2
C:Superfamily: yeast ribosomal protein S30.e

Query Match 76.0%; Score 231; DB 2; Length 68;
Best Local Similarity 75.9%; Pred. No. 8.7e-18;
Matches 44; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KVHGLARAGKVRGQTPKVAQKQKKKTGAKRRMQYNRRFVNVVPTFGKKKGPNNAN 58
Db 9 KVHGLARAGKVRGQTPKVAQKQKKKPRGAHKRLQHNRRFVTAVVVGFGKKRGPNS 66

RESULT 6
T15642
hypotheical protein C26F1.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C:Accession: T15642
R:Geisel, C.; Steillyes, L.; Bradshaw, H.

submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid C26F1.
A:Reference number: 218381
A:Accession: J15642
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-130 <GE1>
A:Cross-references: EMBL:U53148; NID:g1255375; PID:g1255381; PIDN:AB37076.1; GSPDB:GN00
A:Experimental source: strain Bristol N2; clone C26F1
C:Genetics:
A:Gene: CESP:C26F1.4
A:Map position: 5
A:Introns: 27/3; 71/1
C:Superfamily: unaassigned ubiquitin-related proteins; ubiquitin homology

Query Match 74.7%; Score 227; DB 2; Length 130;
Best Local Similarity 76.3%; Pred. No. 4e-11; 9; Indels 0; Gaps 0;
Matches 45; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 KKHGSLARAGKVGOTPPKAAKOEKKKKTKGRAKRMQYRRFVNVVPTFGKKKPNANS 59
Db 72 KKHGSLARAGKVGOTPPKVDKODKKKKGRARFRVQYRRYVNVASGPGKKRGPNS 130

RESULT 7
A1604
ribosomal protein S30 PFB0885W - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 13-Aug-1999
A:Accession: A17604
R:Gardner, M.J.; Tettelin, H.; Carnucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
.; Petter, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A17600; MUID:99021743; PMID:9804551
A:Accession: A17604
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-58 <GAR>
A:Cross-references: GB:AE001422; GB:AE001362; NID:g3845298; PIDN:AAC71966.1; PID:g384530
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0885W
C:Superfamily: yeast ribosomal protein S30.e

Query Match 62.0%; Score 188.5; DB 2; Length 58;
Best Local Similarity 64.4%; Pred. No. 2.4e-13;
Matches 38; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

Qy 1 KKHGSLARAGKVGOTPPKAAKOEKKKKTKGRAKRMQYRRFVNVVPTFGKKKPNANS 59
Db 3 KKHGSLARAGKVGOTPPKPKLDKKKLTGRAKKQLYRRFSD---NGGRKKGPNSKA 58

RESULT 8
T39834
ribosomal protein s30 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
A:Accession: T39834
R:Lyne, M.; Rajandream, M.A.; Barrett, B.G.; Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21884
A:Accession: T39834
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-61 <LYN>
A:Cross-references: EMBL:AL021839; PIDN:CAA17057.2; GSPDB:GN00067; SPDB:SPBC1967.03C
A:Experimental source: strain 972h-; cosmid c19G7
C:Genetics:
A:Gene: SPDB:SPBC1967.03C
A:Map position: 2
A:Introns: 13/3; 56/3

C:Superfamily: yeast ribosomal protein S30.e

Query Match 57.9%; Score 176; DB 2; Length 61;
Best Local Similarity 62.7%; Pred. No. 5.4e-12;
Matches 37; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 1 KKHGSLARAGKVGOTPPKAAKOEKKKKTKGRAKRMQYRRFVNVVPTFGKKKPNANS 59
Db 3 KKHGSLARAGKVGOTPPKVEKEKPKOPKGRAYKRLLYRRFVNVVNTMVGKRRMPPSS 61

RESULT 9
S67074
ribosomal protein S30.e, cytosolic - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein O4725; protein YLR287c-a; protein YOR182c
C:Species: Saccharomyces cerevisiae
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
A:Accession: S67074; S70775; S70776; S70774
R:Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66685
A:Accession: S67074
A:Molecule type: DNA
A:Residues: 1-63 <HUG>
A:Cross-references: EMBL:Z75090; GSPDB:GN00015; MIPS:YOR182C; NID:g1420438; PIDN:CAA99391
A:Experimental source: strain S288C
C:Genetics: YS30B
A:Gene: R.T.; Williams, N.A.; Wettenthal, R.E.H.
J. Biol. Chem. 271, 13549-13553, 1996
A:Title: The yeast homolog of mammalian ribosomal protein S30 is expressed from a duplicate
A:Reference number: S70774; MUID:96278780; PMID:8662789
A:Accession: S70775
A:Molecule type: DNA
A:Residues: 1-63 <BAK>
A:Cross-references: EMBL:U48700; NID:g1256752; PIDN:AAC49317.1; PID:g1256753
A:Accession: YS30A
A:Status: YS30A
A:Accession: S70776
A:Molecule type: mRNA
A:Residues: 1-63 <BAW>
A:Cross-references: EMBL:U48699; NID:g1256750; PIDN:AAC49316.1; PID:g1256751
A:Accession: YS30A
A:Status: YS30A
A:Accession: S70774
A:Molecule type: protein
A:Residues: 2-63 <BA3>
C:Genetics: <YS30B>
A:Gene: SGD:RPS30B; MIPS:YOR182C
A:Cross-references: MIPS:YOR182C; SGD:S0005708
A:Map position: 15R
A:Introns: 1/3
C:Genetics: <YS30A>
A:Gene: SGD:RPS30A; MIPS:YLR287c-a
A:Cross-references: MIPS:YLR287c-a; SGD:S0004278
A:Map position: 12R
A:Introns: 1/3
C:Superfamily: yeast ribosomal protein S30.e
C:Keywords: cytosol; protein biosynthesis; ribosome
P:2-63/Product: ribosomal protein S30.e, cytosolic #status experimental <Mat>

Query Match 57.7%; Score 175.5; DB 1; Length 63;
Best Local Similarity 62.7%; Pred. No. 6.2e-12;
Matches 37; Conservative 6; Mismatches 13; Indels 3; Gaps 1;

Qy 1 KKHGSLARAGKVGOTPPKAAKOEKKKKTKGRAKRMQYRRFVNVVPTFGKKK---GPN 56
Db 3 KKHGSLARAGKVGKOTPPKVEKTEKPKKPGRAVKRLLYRRFVNVVTLVNGKRRMPPGS 61

RESULT 10
S38183
SBA4B protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 08-Sep-1997
A:Accession: S38183

Qy	3	HGSLARAGKVRGQT	PKV-AKQEKKKKKTKRAKRRMQYNRRFVNV	43
		:	:	
Db	4	HGSLTRAGKVRKQT	PLRPAKQ--KKNYPPRLKNRLKYQVRIEKV	45
		:	:	
RESULT 13				
	573991	ribosomal protein L4 - Mycoplasma pneumoniae (strain ATCC		
N;	Alternate names:	hypothetical protein VxpSP77_of212		
C;	Species:	Mycoplasma pneumoniae		
A;	Variety:	ATCC 29342		
C;	Date:	27-Feb-1997 #sequence_revision 25-Apr-1997 #text_		
C;	Accession:	S73991		
R;	Himmeldich, R.;	Hilbert, H.;		
		Plegens, H.;		
		Pirkle, E.;		
		L		
	Nucleic Acids Res.	24, 4420-4449, 1996		
A;	Title:	Complete sequence analysis of the genome of the		
A;	Reference number:	S73327; MUID:97105985; PMID:8948633		
A;	Accession:	S73991		
A;	Status:	nucleic acid sequence not shown; translation not		
A;	Molecule type:	DNA		
A;	Residues:	1-212 <HIM>		
A;	Cross-references:	EMBL:AE000061; GB:U00089; NID:G1674333		
A;	Note:	The nucleotide sequence was submitted to the EMBL		
C;	Genetics:			
A;	Gene:	rplD		
A;	Genetic code:	SGC3		
C;	Superfamily:	Escherichia coli ribosomal protein L4		
C;	Keywords:	protein biosynthesis; ribosome		
	Query Match	21.7%;	Score 66;	DB 2;
	Best Local Similarity	37.0%;	Pred. No. 7, 1;	
	Matches	20;	Conservative	7; Mismatches 21;
				Indels 0;
Qy	5	SLARAGKVRGQT	PKVAKQEKKKKKTKRAKRRMQYNRRFVNVVPTFGK	
		:	:	
Db	51	SILTKGEVRGG	---GKKPKYKQKHTGKARQGSRNPHFVGGGIVFGP	
		:	:	

A:3340
 nucleocapsid protein - murine hepatitis virus (strain A59)
 C:Species: murine hepatitis virus, MHV
 A:Variety: strain A59
 C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 16-Jul-1999
 C:Accession: A45340; A04023; A47310
 R:Parker, M.M.; Masters, P.S.
 Virology 179, 463-468, 1990
 A:Title: Sequence comparison of the N genes of five strains of the coronavirus mouse hepa
 A:Reference number: A45340; MUID:91021052; PMID:2171216
 A:Accession: A45340
 A:Molecule type: Genomic RNA
 A:Residues: 1-454 <PAR>
 A:Cross-references: GB:M35256; NID:g331826; PIDN:AAA46447.1; PID:g331827
 R:Armstrong, J.; Smeekens, S.; Rottier, P.
 Nucleic Acids Res. 11, 883-891, 1983
 A:Title: Sequence of the nucleocapsid gene from murine coronavirus MHV-A59.
 A:Reference number: A04023; MUID:83188908; PMID:6687635
 A:Accession: A04023
 A:Molecule type: Genomic RNA
 A:Residues: 1-108, 'AVLLKHLMGSRNSYPCDGFITLTAQGMLEPVMETALKES', 'SGLQAKRTPIPALILSKGTQAVMR'
 A:Cross-references: GB:X00509; GB:J02252; NID:958965
 R:Schaad, M.C.; Baric, R.S.
 Virology 196, 190-198, 1993
 A:Title: Evidence for new transcriptional units encoded at the 3' end of the mouse hepa
 A:Reference number: A47310; MUID:93362405; PMID:8395114
 A:Accession: A47310
 A:Molecule type: mRNA
 A:Residues: 301-454 <SCH>
 A:Cross-references: GB:S64884; NID:g408334; PIDN:AAB27902.1; PID:g408335
 A:Note: sequence extracted from NCBI backbone (NCBIN:136580, NCBIPI:136581)
 C:Genetics:
 A:Gene: N

C:Superfamily: coronavirus nucleocapsid protein
C:Keywords: glycoprotein; nucleocapsid
F:409,422/Binding site: carbohydrate (Asn) (covalent) #status predicted

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 3, 2002, 14:30:48 ; Search time 11 Seconds
(without alignments)
222.464 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 304
Sequence: 1 KVHSLARAGKVRGQTPKVA.....RRFNVVPTFGKKKGNANS 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	304	100.0	59 1 RS30_HUMAN	Q05472 homo sapien
2	254	83.6	59 1 RS30_ORYLA	Q9WY0 Oryzias lat
3	231	76.0	62 1 RS30_ARATH	P49689 arabidopsis
4	188.5	62.0	58 1 RS30_PLAFA	O96269 plasmodium
5	176	57.9	61 1 RS30_SCHPO	O42952 schizosacch
6	175.5	57.7	62 1 RS30_YEAST	Q12087 saccharomyc
7	91.5	30.1	50 1 RS30_AERPE	Q9Y9C9 aeropyrum p
8	67.5	22.2	454 1 NCAL_CVMAS	P03416 murine coro
9	66	21.7	212 1 RLA_MYCPN	P75579 mycoplasma
10	64.5	21.2	454 1 NCAL_CVMAS	P18448 murine coro
11	64.5	21.2	454 1 NCAP_CVMS	P18447 murine coro
12	64.5	21.2	454 1 NCAP_CVMS	P18449 murine coro
13	64.5	21.2	454 1 NCAP_CVMS	Q02915 rat coronav
14	64.5	21.2	455 1 NCAP_CVMS	P18446 murine coro
15	64.5	21.2	455 1 NCAP_CVMS	P03417 murine coro
16	63	20.7	399 1 CC37_DROVI	Q24740 drosophila
17	62.5	20.6	206 1 HMG2_CHICK	P26584 gallus gall
18	60.5	19.9	617 1 SG2_MOUSE	Q03517 mus musculu
19	60.5	19.9	1362 1 BRD4_HUMAN	O60885 homo sapien
20	60	19.7	439 1 AKR_ARATH	Q05753 arabidopsis
21	60	19.7	1064 1 ISKS_HUMAN	Q9N938 homo sapien
22	59.5	19.6	205 1 RRA_EUGAR	P27418 euglena gra
23	59.5	19.6	752 1 DR81_YEAST	P32892 saccharomyc
24	58	19.4	286 1 YLU2_CAEEL	P34396 caenorhabdi
25	58	19.1	208 1 HMG2_HUMAN	P26583 homo sapien
26	58	19.1	209 1 HMG2_PIG	P17741 sus scrofa
27	58	19.1	774 1 GLYB_PLAFA	P02895 plasmodium
28	57.5	18.9	211 1 RLA_MYCPN	P47398 mycoplasma
29	57.5	18.9	555 1 PERP_HUMAN	P14222 homo sapien
30	57.5	18.9	862 1 VGO1_HSV1	Q00132 iccatalinid h
31	57	18.8	269 1 HMG2_MOUSE	P30681 mus musculu
32	57	18.8	209 1 HMG2_RAT	P52825 ratius norv
33	57	18.8	685 1 SNWA_DICDI	P54705 dictyosteti

34	57	18.8	785 1 MUS2_BACHD	O9K8A0 bacillus ha
35	56.5	18.6	372 1 CIS2_BACCU	P39120 bacillus bu
36	56	18.4	150 1 VPS_BPP2	P36934 bacterioph
37	56	18.4	174 1 YD5A_SCHPO	O14185 schizosacch
38	55.5	18.3	187 1 PENK_SCHPO	O28409 felis silve
39	55.5	18.3	233 1 YQAL_BACCU	P45909 bacillus bu
40	55	18.1	11 1 RS30_ONCMY	P83328 oncorhynch
41	55	18.1	121 1 H2B_ASTRU	P02286 asterias ru
42	55	18.1	747 1 DIL2_HUMAN	O9U1W0 homo sapien
43	55	18.1	2059 1 TEGU_HSV1	P52362 human herpes
44	54.5	17.9	110 1 Y225_METYA	O60284 methanococ
45	54.5	17.9	209 1 R44_MYCGA	O52333 mycoplasma

ALIGNMENTS

RESULT 1
ID RS30_HUMAN STANDARD; PRT; 59 AA.
AC Q05472; Q95261;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 40S ribosomal protein S30.
GN PAU.
OS Homo sapiens (Human).
OS Mus musculus (Mouse).
OS Rattus norvegicus (Rat).
OS Citellus griseus (Chinese hamster), and
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606, 10090, 10116, 10029, 9823;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=92412144; PubMed=1326960;
RA Kas K., Michiels L., Merregaert J.;
RT "Genomic structure and expression of the human fau gene: encoding the
RT ribosomal protein S30 fused to a ubiquitin-like protein.";
RT Biochem. Biophys. Res. Commun. 187:927-933(1992).
[2]
RP SEQUENCE FROM N.A.
RC SPECIES=Human, and Mouse;
RX MEDLINE=93368957; PubMed=8395683;
RA Michiels L., Van der Raaij-MacLeod E., van Haeseelt F., Kas K.,
RA Merregaert J.;
RT "faa cDNA encodes a ubiquitin-like-S30 fusion protein and is
RT expressed as an antisense sequence in the Finkel-Biskis-Reilly murine
RT sarcoma virus.";
RT Oncogene 8:2537-2546(1993).
[3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-18.
RC SPECIES=Rat; STRAIN=Sprague-Dawley; TISSUE=liver;
RX MEDLINE=93352612; PubMed=8394356;
RA Olvera J., Wool I.G.;
RT "The carboxyl extension of a ubiquitin-like protein is rat ribosomal
RT protein S30.";
RT J. Biol. Chem. 268:17967-17974(1993).
[4]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=BALB/C;
RX MEDLINE=95241522; PubMed=7724584;
RA Nakamura M., Xavier R.M., Tanigawa Y.;
RT "Molecular cloning and characterization of a cDNA encoding monoclonal
RT non-specific suppressor factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:3463-3467(1995).
[5]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=BALB/C; TISSUE=liver;
RX MEDLINE=95293388; PubMed=7774934;
RA Casteels D., Poirier C., Guenet J.-L., Merregaert J.;

```
RT "The mouse Fau gene: genomic structure, chromosomal localization, and
RL characterization of two retropseudogenes.";
RN Genomics 25:291-294 (1995).
RP [6]
RC SEQUENCE FROM N.A.
RC SPECIES=C. griseus;
RA Rossmann T.G., Wang Z.;
RN Submitted (DSC-1995) to the EMBL/GenBank/DBJ databases.
RN [7]
RN SEQUENCE FROM N.A.
RP SPECIES=Pig; TISSUE=Uterus;
RX MEDLINE=9724440; PubMed=9089280;
RA Chwetroff S., D'Andrea S.;
RT "Ubiquitin is physiologically induced by interferons in luminal
RT epithelium of porcine uterine endometrium in early pregnancy: global
RT RT-PCR cDNA in place of RNA for differential display screening.";
RL FEBS Lett. 405:148-152 (1997).
CC -!- MISCELLANEOUS: THIS RIBOSOMAL PROTEIN IS SYNTHESIZED AS A
CC C-TERMINAL EXTENSION PROTEIN (CEP) OF A UBIQUITIN-LIKE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; X65921; CAA46714.1; ALT_INIT.
DR EMBL; X65923; CAA46716.1; ALT_INIT.
DR EMBL; X62671; CAA44546.1; -.
DR EMBL; X62671; CAA44545.1; ALT_INIT.
DR EMBL; X65922; BAA05655.1; ALT_INIT.
DR EMBL; D26610; BAA05655.1; ALT_INIT.
DR EMBL; L31715; ABA91564.1; ALT_INIT.
DR EMBL; U41499; ABA83776.1; ALT_INIT.
DR EMBL; U72543; AAB52915.1; ALT_INIT.
DR PIR; JC1278; JC1278.
DR Genew; HGNC:3597; FAU.
DR MIW; L34690; -.
DR MGD; MGI:102547; Fau.
KW Ribosomal protein.
SQ SEQUENCE 59 AA; 6648 MW; 012AC1F555B01A4 CRC64;

Query Match 100.0%; Score 304; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 3.2e-29;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVHGLARAGKVRGQTPKVAQKKKKTKGAKRMQYNRRFVNVVPTFGKKKGPNANS 59
Db 1 KVHGLARAGKVRGQTPKVAQKKKKTKGAKRMQYNRRFVNVVPTFGKKKGPNANS 59

RESULT 2
RS30 ORYLA STANDARD; PRT; 59 AA.
AC Q9W6Y0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S30.
GN FAU OR RPS30.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN SEQUENCE FROM N.A.
RP MEDLINE=20070552; PubMed=10603084;
RX Heinrich T., Wittbrodt J.;
```

```
RT "An in situ hybridization screen for the rapid isolation of
RT differentially expressed genes.";
RL Dev. Genes Evol. 210:28-33 (2000).
CC -!- MISCELLANEOUS: THIS RIBOSOMAL PROTEIN IS SYNTHESIZED AS A
CC C-TERMINAL EXTENSION PROTEIN (CEP) OF A UBIQUITIN-LIKE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ238274; CAB40969.1; ALT_INIT.
KW Ribosomal protein.
SQ SEQUENCE 59 AA; 6660 MW; E91B9C088C7772CF CRC64;

Query Match 83.6%; Score 254; DB 1; Length 59;
Best Local Similarity 83.1%; Pred. No. 2.3e-23;
Matches 49; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KVHGLARAGKVRGQTPKVAQKKKKTKGAKRMQYNRRFVNVVPTFGKKKGPNANS 59
Db 1 KVHGLARAGKVRGQTPKVAQKKKKTKGAKRMQYNRRFVNVVPTFGKKKGPNANS 59

RESULT 3
RS30 ARATH STANDARD; PRT; 62 AA.
ID RS30_ARATH STANDARD; PRT; 62 AA.
AC P49689; O82203; Q9M0E4;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S30.
GN (RPS30A OR AT2G19750 OR P6F22.22) AND
GN (RPS30B OR AT4G29390 OR F1AI3.210) AND
GN (RPS30C OR AT5G56670 OR MIK19.12).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RA Lebas M., Regad F., Lescure B.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A. (RPS30A).
RP STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768 (1999).
RN [3]
RN SEQUENCE FROM N.A. (RPS30B).
RP STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
RA Harris B., Ansoerge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
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RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohetel J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCallagh B., Bilham L., Robben J.,
 RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandebussche F.,
 RA Braeken M., Welfjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weizenecker T., Botte G., Rameberger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
 RA Moorjman P., Klein Lankhorst R., Rose M., Hauf J., Koester P.,
 RA Bernier S., Hempel S., Feldpausch M., Lambirth S., Van den Daele H.,
 RA De Keyser A., Buysheert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay K., Mayes R.,
 RA Petrett A., Rajandream M.A., Lyne M., Benes V., Reckmann S.,
 RA Borrova D., Bioecker H., Scharfe M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Farman B., Granderath K., Danner D., Herzi A.,
 RA Neumann S., Agirion A., Vitale D., Liguori R., Piravandi E.,
 RA Maesene O., Quigley F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chetdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vanderbol M., Barques M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Baetide M., Habermann K.,
 RA Parnell L., Dedha N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Speth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Anonou B., Zidan M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Macero A., Shah R.,
 RA Swaby J.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
 RA Gravat S., Shohdy N., Hasegawa A., Hamed A., Lofth M., Johnson A.,
 RA Chen E., Marra M., Martensen R., McCombe W.R.,
 RA "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RT thaliana."
 RT Nature 402:769-777(1999).
 RL [4]
 RN SEQUENCE FROM N.A. (RPS30C).
 RP STRAIN=cv. Columbia;
 RC MEDLINE=98403884; PubMed=9734815;
 RX KORANI H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
 RA Tabata S.,
 RA "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
 RT Sequence features of the regions of 1,367,185 bp covered by 19
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:203-216(1998).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,
 RT "RIKEN Arabidopsis full length cDNA clones (RAPFs) sequenced by the
 RT SSP consortium (Salk/Stanford/PECC)."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL; Z26869; CAA81482.1; -;
 DR EMBL; AC006169; AAC62141.2; -;
 DR EMBL; AL161574; CAB79697.1; -;
 DR EMBL; AL096692; -; NOT_ANNOTATED_CDS.
 DR EMBL; AB013392; BAB09885.1; -;

DR EMBL; AY052341; AAK96533.1; -;
 DR EMBL; AY061910; AAL31237.1; -;
 KW Ribosomal protein, Multigene family.
 FT CONFLICT 17 19 OTR -> RHQ (IN REF. 1).
 SQ SEQUENCE 62 AA; 6887 MW; 95D8F3EB72F53F33 CRC64;
 Query Match 76.0%; Score 231; DB 1; Length 62;
 Best Local Similarity 75.9%; Pred. No. 1.2e-20;
 Matches 44; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
 QY 1 KYHGSILARAGKVRGQTPKVAKOEKKKKTKGRAKRQVYRRPNNVPTGKKKGPAN 58
 DB 3 KYHGSILARAGKVRGQTPKVAKODKKKKRGRHAKRLQHNRRFVTAVVGFGKKRPNSS 60
 RESULT 4
 RS30_PLAFA STANDARD; PRT; 58 AA.
 ID RS30_PLAFA
 AC O96269;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 40S ribosomal protein S30.
 GN RPS30 OR PFB0885W.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99021743; PubMed=9804551;
 RA Gardner M.J., Tetteijn H., Carucci D.J., Cummings L.M., Aravind L.,
 RA Koonin E.V., Shallow S., Mason T., Yu K., Fujii C., Pederson J.,
 RA Shen K., Jing J., Asencio C., Lai Z., Schwartz D.C., Petrea M.,
 RA Salberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
 RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.,
 RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
 RT falciparum."
 RL Science 282:1126-1132(1998).
 CC -I- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 DR EMBL; AE001422; AAC71966.1; -;
 DR KW Ribosomal protein.
 SQ SEQUENCE 58 AA; 6488 MW; 525675AE74D04ESF CRC64;
 Query Match 62.0%; Score 188.5; DB 1; Length 58;
 Best Local Similarity 64.4%; Pred. No. 1.1e-15;
 Matches 38; Conservative 8; Mismatches 10; Indels 3; Gaps 1;
 QY 1 KYHGSILARAGKVRGQTPKVAKOEKKKKTKGRAKRQVYRRPNNVPTGKKKGPAN 59
 DB 3 KYHGSILARAGKVRGQTPKVAKODKKKKRGRHAKRLQHNRRFVTAVVGFGKKRPNSS 60
 RESULT 5
 RS30_SCHPO STANDARD; PRT; 61 AA.
 ID RS30_SCHPO
 AC O42952; O14314;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 40S ribosomal protein S30.
 GN RPS30A OR RPS30 OR SPAC19B12.04 OR (RPS30B OR SPAC19G7.03C).
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OK NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=9910339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Hatakeyama Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anai A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudo Y.,
 RA Yamazaki J., Kusuda N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sake Y., Kikuchi H.,
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Ref. 6:83-101(1999).
 CC -1- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 DR EMBL; AP00063; BAA8121.1;
 KM Ribosomal protein; Complete proteome.
 SQ SEQUENCE 50 AA; 5701 MW; 346A9DABD4E67DCF CRC64;
 Query Match 30.1%; Score 91.5; DB 1; Length 50;
 Best Local Similarity 52.3%; Pred. No. 0.00021;
 Matches 23; Conservative 5; Mismatches 13; Indels 3; Gaps 2;
 Oy 3 HGSILARAGVGGOTPKV-AKOEKKKKTKGRAKRMQYRRFVNV 45
 Db 4 HGSILKAGVKKOTPRPAQ-KKAYPRRLKRLKYQVRIEKV 45
 RESULT 8
 NCBI_CVMA5 STANDARD; PRT; 454 AA.
 AC P03416;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Nucleocapsid protein (Version 1).
 GN N.
 OS Murine coronavirus MHV (strain A59).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 OC NCBI_TaxID=11142;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83168908; PubMed=6667635;
 RA Armstrong J., Smeekens S., Rottier P.J.M.,
 RA van der Zeijst B.A.M.;
 RT "Cloning and sequencing of the nucleocapsid and E1 genes of
 RT coronavirus";
 RL (In) Rottier P.J.M., van der Zeijst B.A.M., Spaan W.J.M.,
 RL Horzinek W. (eds.);
 RL Molecular biology and pathogenesis of coronaviruses, pp.155-162,
 RL Plenum Press, New York (1984).
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 CC -----
 DR EMBL; X00509; CAA25198.1;
 DR PIR; A04023; VHI9M.
 DR InterPro; IPR001218; Corona_nucleocap.
 DR Pfam; PF00937; Corona_nucleocap.1.
 KW Nucleocapsid.
 SQ SEQUENCE 454 AA; 49728 MW; 4FD75D69BAC822F CRC64;
 Query Match 22.2%; Score 67.5; DB 1; Length 454;
 Best Local Similarity 38.2%; Pred. No. 1.2;
 Matches 21; Conservative 7; Mismatches 24; Indels 3; Gaps 2;
 Oy 6 LARAGVGGOTPKVAKOEKK-KTGRAKRMQYRRFVNVPTFGKKGPAN 58
 Db 242 LAKLGKDNQPPQVTKOSAKYRKILNKPRKRTNKKCPVQCGG-KRGRPN 295
 RESULT 9
 NCBI_CVMA5 STANDARD; PRT; 212 AA.
 AC P75579;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L4.
 GN RPLD OR MP166 OR MP665.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OC NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=8948633;
 RA Himmelfeich R., Hilbert H., Piagens H., Pirkl E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY AND SPECIFICALLY TO 23S
 CC -1- RNA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE L4P FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 DR EMBL; AE00061; AAB96313.1;
 DR InterPro; IPR002136; Ribosomal_L4/L1E.
 DR Pfam; PF00573; Ribosomal_L4; 1.
 KW Ribosomal protein; RNA-binding; Complete proteome.
 SQ SEQUENCE 212 AA; 58421C03A2754D08 CRC64;
 Query Match 21.7%; Score 66; DB 1; Length 212;
 Best Local Similarity 37.0%; Pred. No. 0.84;
 Matches 20; Conservative 7; Mismatches 21; Indels 6; Gaps 2;
 Oy 5 SLARAGVGGOTPKVAKOEKKKKTKGRAKRMQYRRFVNVPTFGKKGPAN 58
 Db 51 SLITKGEVRGG---CKPKYKQHTKAKAGSTRNHFVCGGIVFQPK--PNNR 98
 RESULT 10
 NCBI_CVMA5 STANDARD; PRT; 454 AA.
 AC P18448;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)

```
DE Nucleocapsid protein (Version 2).
GN N.
OS Murine coronavirus MHV (strain A59).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11142;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021052; PubMed=2171216;
RA Parker M.M., Masters P.S.;
RT "Sequence comparison of the N genes of five strains of the
RT coronavirus mouse hepatitis virus suggests a three domain structure
RT for the nucleocapsid protein.";
RL Virology 179:463-468(1990).
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CC -----
DR EMBL; M35255; AAA46468.1; -
DR PIR; C45340; C45340.
DR InterPro; IPR001218; Corona_nucleocap.
DR Pfam; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 454 AA; 49587 MW; 4992187AB0EB131E CRC64;

Query Match 21.2%; Score 64.5; DB 1; Length 454;
Best Local Similarity 36.4%; Pred. No. 2.7;
Matches 20; Conservative 8; Mismatches 24; Indels 3; Gaps 2;

Oy 6 LARAGKVRGQTPKVAQKQK--KKKTGAKRMOYNNRRFVNVVPTFGKKKGPNNAN 58
Db 242 LAKLGDAGQPKQVTKQSAKEVRQKILNKPRQKTPNKQCPVQOCFG-KRGPNQN 295

RESULT 11
NCAP_CVMS STANDARD; PRT; 454 AA.
ID NCAP_CVMS
AC P1847;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Murine coronavirus MHV (strain 3).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11140;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021052; PubMed=2171216;
RA Parker M.M., Masters P.S.;
RT "Sequence comparison of the N genes of five strains of the
RT coronavirus mouse hepatitis virus suggests a three domain structure
RT for the nucleocapsid protein.";
RL Virology 179:463-468(1990).
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CC -----
DR EMBL; M35254; AAA46444.1; -
DR PIR; B45340; B45340.
DR InterPro; IPR001218; Corona_nucleocap.
DR Pfam; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid protein (Version 2).
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KW Nucleocapsid.
SQ SEQUENCE 454 AA; 49687 MW; 9C46DB2317E3A849 CRC64;

Query Match 21.2%; Score 64.5; DB 1; Length 454;
Best Local Similarity 36.4%; Pred. No. 2.7;
Matches 20; Conservative 8; Mismatches 24; Indels 3; Gaps 2;

Oy 6 LARAGKVRGQTPKVAQKQK--KKKTGAKRMOYNNRRFVNVVPTFGKKKGPNNAN 58
Db 242 LAKLGDAGQPKQVTKQSAKEVRQKILNKPRQKTPNKQCPVQOCFG-KRGPNQN 295

RESULT 12
NCAP_CVMS STANDARD; PRT; 454 AA.
ID NCAP_CVMS
AC P18449;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Murine coronavirus MHV (strain S).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11145;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021052; PubMed=2171216;
RA Parker M.M., Masters P.S.;
RT "Sequence comparison of the N genes of five strains of the
RT coronavirus mouse hepatitis virus suggests a three domain structure
RT for the nucleocapsid protein.";
RL Virology 179:463-468(1990).
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CC -----
DR EMBL; M35256; AAA46447.1; -
DR PIR; A45340; A45340.
DR InterPro; IPR001218; Corona_nucleocap.
DR Pfam; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 454 AA; 49729 MW; 7C4978F20954A227 CRC64;

Query Match 21.2%; Score 64.5; DB 1; Length 454;
Best Local Similarity 36.4%; Pred. No. 2.7;
Matches 20; Conservative 8; Mismatches 24; Indels 3; Gaps 2;

Oy 6 LARAGKVRGQTPKVAQKQK--KKKTGAKRMOYNNRRFVNVVPTFGKKKGPNNAN 58
Db 242 LAKLGDAGQPKQVTKQSAKEVRQKILNKPRQKTPNKQCPVQOCFG-KRGPNQN 295

RESULT 13
NCAP_CVMS STANDARD; PRT; 454 AA.
ID NCAP_CVMS
AC Q02915;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Rat coronavirus (strain 681) (SDAV) (Sialodacryoadenitis virus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=33740;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE=93174973; PubMed=8438589;
RA Kunita S., Mori M., Terada E.;
RT "Sequence analysis of the nucleocapsid protein gene of rat
RL coronavirus SDAV-681."
RT Virology 193:520-523(1993).
CC -1- SIMILARITY: TO NUCLEOCAPSID PROTEINS OF MURINE CORONAVIRUS MHV.
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CC -----
DR EMBL: D10760; BAA01591.1; -.
DR PIR: A45396; A45396.
DR InterPro: IPR001218; Corona_nucleocap.
DR Pfam: PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
FT DOMAIN 1 16 SER-RICH.
FT 194 220 SER-RICH.
SQ SEQUENCE 454 AA; 49437 MW; 247184B05D6CD96D CRC64;

Query Match 21.2%; Score 64.5; DB 1; Length 454;
Best Local Similarity 36.4%; Pred. No. 2.7;
Matches 20; Conservative 8; Mismatches 24; Indels 3; Gaps 2;

Qy 6 LARAGVRCQTPKVAKEKK--KKKTGRAKRRMYNRRFNVVPTFGKKKGGPNAN 58
Db 242 LAKLGKDAQPKQVTKQSAKEVRQKILNKPRQKRTPNKQCPVQOCFG-KRGPNN 295

RESULT 14
ID NCAP_CVWJH STANDARD; PRT; 455 AA.
AC P18446;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Murine coronavirus MHV (strain 1).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021052; PubMed=2171216;
RA Parker M.M., Masters P.S.;
RT "Sequence comparison of the N genes of five strains of the
RT coronavirus mouse hepatitis virus suggests a three domain structure
RL for the nucleocapsid protein."
RL Virology 179:463-468(1990).
CC -----
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CC -----
DR EMBL: M35253; AAA46439.1; -.
DR PIR: D45340; D45340.
DR InterPro: IPR001218; Corona_nucleocap.
DR Pfam: PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 455 AA; 49694 MW; 382DBE4DA264BFF CRC64;

Query Match 21.2%; Score 64.5; DB 1; Length 455;
Best Local Similarity 36.4%; Pred. No. 2.7;
Matches 20; Conservative 8; Mismatches 24; Indels 3; Gaps 2;

```

```

Qy 6 LARAGVRCQTPKVAKEKK--KKKTGRAKRRMYNRRFNVVPTFGKKKGGPNAN 58
Db 242 LAKLGKDAQPKQVTKQSAKEVRQKILNKPRQKRTPNKQCPVQOCFG-KRGPNN 295

RESULT 15
ID NCAP_CVWJH STANDARD; PRT; 455 AA.
AC P03417;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nucleocapsid protein.
GN N.
OS Murine coronavirus MHV (strain JHM).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11144;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8372950; PubMed=6308569;
RA Skinner M.A., Siddell S.G.;
RT "Coronavirus JHM: nucleotide sequence of the mRNA that encodes
RT nucleocapsid protein."
RL Nucleic Acids Res. 11:5045-5054(1983).
CC -----
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CC -----
DR EMBL: X00990; CA425497.1; -.
DR PIR: A04024; VHIMJ.
DR InterPro: IPR001218; Corona_nucleocap.
DR Pfam: PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 455 AA; 49714 MW; 36FC529D1272B5BE CRC64;

Query Match 21.2%; Score 64.5; DB 1; Length 455;
Best Local Similarity 36.4%; Pred. No. 2.7;
Matches 20; Conservative 8; Mismatches 24; Indels 3; Gaps 2;

Qy 6 LARAGVRCQTPKVAKEKK--KKKTGRAKRRMYNRRFNVVPTFGKKKGGPNAN 58
Db 242 LAKLGKDAQPKQVTKQSAKEVRQKILNKPRQKRTPNKQCPVQOCFG-KRGPNN 295

Search completed: December 3, 2002, 14:32:16
Job time : 12 secs

```


GenCore version 5.1.3
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OW protein - protein search, using SW model

Run on: December 3, 2002, 14:30:48 ; Search time 29 Seconds
(without alignments)
419.199 Million cell updates/sec

Title: US-09-424-815E-1
Perfect score: 304
Sequence: 1 KVHGLARAGKVRGQTPKVA.....RRFVVVPTFGKKKGPNNAS 59

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteria:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	304	100.0	133	4	Q9H5V4	Q9H5V4 homo sapien
2	304	100.0	133	11	Q9J24	Q9J124 mus musculus
3	304	100.0	137	11	Q920W8	Q920W8 mus musculus
4	304	100.0	137	11	Q920W7	Q920W7 mus spicile
5	304	100.0	137	11	Q91V99	Q91V99 mus musculus
6	288	94.7	133	13	Q90YPI	Q90YPI ictaluruss p
7	269	88.5	131	5	Q962Q1	Q962Q1 spodoptera
8	263	86.5	132	5	Q9VDH8	Q9VDH8 drosofila
9	231	76.0	62	10	Q9M0E4	Q9M0E4 arabidopsis
10	227	74.7	130	5	Q18231	Q18231 caenorhabdi
11	112	36.8	230	4	Q15351	Q15351 homo sapien
12	104.5	34.4	52	17	Q972H4	Q972H4 sulfolobus
13	101.5	33.4	55	17	Q971W4	Q971W4 sulfolobus
14	95	31.2	59	5	Q8SR05	Q8SR05 encephalito
15	87.5	28.8	55	17	Q8ZV51	Q8ZV51 pyrobaculum
16	65	21.4	219	10	Q91G56	Q91G56 oryza sativa

17	64.5	21.2	425	12	Q83357	Q83357 murine hepa
18	64.5	21.2	451	12	Q83359	Q83359 murine hepa
19	64.5	21.2	454	12	Q83358	Q83358 murine hepa
20	64.5	21.2	454	12	Q9WCD0	Q9WCD0 rat coronav
21	64.5	21.2	454	12	Q9J3E2	Q9J3E2 murine hepa
22	64.5	21.2	455	12	Q83360	Q83360 murine hepa
23	64.5	21.2	455	12	Q9QC29	Q9QC29 murine hepa
24	64.5	21.2	457	12	Q08614	Q08614 murine hepa
25	64	21.1	425	16	Q8YX55	Q8YX55 anabena sp
26	63.5	20.9	451	12	Q9J3F6	Q9J3F6 murine hepa
27	63.5	20.9	451	12	Q72588	Q72588 murine hepa
28	63.5	20.9	451	12	Q9PY96	Q9PY96 murine hepa
29	63.5	20.9	1510	5	Q25920	Q25920 plasmodium
30	63	20.7	260	10	Q9LG29	Q9LG29 arabidopsis
31	63	20.7	290	4	Q99463	Q99463 homo sapien
32	63	20.7	421	5	Q9BL55	Q9BL55 caenorhabdi
33	63	20.7	517	10	Q9LKR2	Q9LKR2 arabidopsis
34	62.5	20.6	454	12	Q9IKC6	Q9IKC6 rat saloda
35	62	20.4	467	16	Q8R617	Q8R617 t hypotheti
36	62	20.4	917	5	Q9VBX5	Q9VBX5 dicophylla
37	61.5	20.2	171	10	Q9LDA1	Q9LDA1 oryza sativ
38	61.5	20.2	836	11	Q9WY8	Q9WY8 rattus norv
39	61	20.1	317	5	Q9U613	Q9U613 atemia san
40	60.5	19.9	351	11	Q9CW80	Q9CW80 mus musculu
41	60.5	19.9	731	4	Q60433	Q60433 homo sapien
42	60	19.7	115	11	Q64390	Q64390 rattus norv
43	60	19.7	435	10	Q940Y0	Q940Y0 arabidopsis
44	60	19.7	521	3	Q42650	Q42650 echinosach
45	60	19.7	893	3	Q8WZ55	Q8WZ55 neurospora

ALIGNMENTS

RESULT 1

Q9H5V4 PRELIMINARY; PRT; 133 AA.
AC Q9H5V4;
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA: FLJ22986 fls, clone KAT11742.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Ohtsuka M., Nishii T., Shibahara T., Tanaka T.,
RA Nakamura Y., Iwagaki T., Sugano S.,
RT "NEO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK026639; BAB15515.1; -
DR HSSP; P02248; IUBI.
DR InterPro; IPR006626; Ubiquitin.
DR Pfam; PF00240; ubiquitin.1.
DR PRINTS; PR00348; Ubiquitin.
DR SMART; SM00213; UBO; 1.
DR PROSITE; PS00299; Ubiquitin_1; 1.
DR PROSITE; PS0053; Ubiquitin_2; 1.
SQ SEQUENCE 133 AA; 14390 MW; 5D2F81F2A3558559 CRC64;

Query Match 100.0%; Score 304; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 4.8e-30;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGLARAGKVRGQTPKVAKKKKKTKGRARRRFRFVVVPTFGKKKGPNNAS 59
DB 75 KVHGLARAGKVRGQTPKVAKKKKKTKGRARRRFRFVVVPTFGKKKGPNNAS 133
RESULT 2

DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Fau protein (Fragment).
 CN FAU.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VARIOUS STRAINS;
 RA Liu Y., Kitano T., Koide T., Shirosaki T., Moriaki K., Saitou N.;
 RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
 RT Five Mus musculus subspecies.";
 RL Submitted (FE8-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB030884; BAB6608.1; -;
 DR EMBL; AB030885; BAB6609.1; -;
 DR EMBL; AB030887; BAB6611.1; -;
 DR EMBL; AB030888; BAB6612.1; -;
 DR EMBL; AB030889; BAB6613.1; -;
 DR EMBL; AB030900; BAB6614.1; -;
 DR EMBL; AB030911; BAB6615.1; -;
 DR EMBL; AB030921; BAB6616.1; -;
 DR InterPro; IPR000626; Ubiquitin.
 DR Pfam; PF00240; Ubiquitin.1.
 DR PROSITE; PS00299; UBIQUITIN_1; UNKNOWN_1.
 DR PROSITE; PS0053; UBIQUITIN_2; 1.
 FT NON_TER
 SQ SEQUENCE 137 AA; 14787 MW; 57099FF7065D8628 CRC64;

Query Match 100.0%; Score 304; DB 11; Length 137;
 Best Local Similarity 100.0%; Pred. No. 5e-30; Indels 0; Gaps 0;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVGSLARAGKVGQTPKVAKEKKKKTGRARRMQYNRRFVNVVPTFGKKKGNPNS 59
 Db 79 KVGSLARAGKVGQTPKVAKEKKKKTGRARRMQYNRRFVNVVPTFGKKKGNPNS 137

RESULT 6
 Q90YP1 PRELIMINARY; PRT; 133 AA.
 AC Q90YP1;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DE 40S ribosomal protein S30.
 OS Ictaelurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurine.
 OX NCBI_TaxId=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Karel A., Patterson A., Feng J., Liu Z.J.;
 RT "Translational machinery of channel catfish: I. A transcriptomic
 RT approach to the analysis of 32 40S ribosomal protein genes and their
 RT expression.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF402841; AAK95215.1; -;
 DR InterPro; IPR000626; Ubiquitin.
 DR Pfam; PF00240; Ubiquitin.1.
 DR PROSITE; PS0053; UBIQUITIN_2; 1.
 KW Ribosomal protein.
 SQ SEQUENCE 133 AA; 14504 MW; 62036B0E72C5CAC CRC64;

Query Match 94.7%; Score 288; DB 13; Length 133;
 Best Local Similarity 94.9%; Pred. No. 4.6e-28; Indels 0; Gaps 0;
 Matches 56; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 KVGSLARAGKVGQTPKVAKEKKKKTGRARRMQYNRRFVNVVPTFGKKKGNPNS 59

Db 75 KVGSLARAGKVGQTPKVAKEKKKKTGRARRMQYNRRFVNVVPTFGKKKGNPNS 133
 RESULT 7
 Q96201 PRELIMINARY; PRT; 131 AA.
 AC Q96201;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Ribosomal protein S30 (Fall armyworm).
 OS Spodoptera frugiperda (Fall armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuidae; Noctuidae; Amphipyridae; Spodoptera.
 OX NCBI_TaxId=7108;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Landais I., Ogliastro M., Mita K., Nohata J., Lopez-Ferber M.,
 RA Duonot-Cerutti M., Fournier P., Devauchelle G.;
 RT "Full-length ribosomal protein sequence from an EST library of
 RT Spodoptera frugiperda cells (Sf9).";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF400225; AAK92197.1; -;
 SQ SEQUENCE 131 AA; 14314 MW; 03AEAD0E31EBC1B04 CRC64;

Query Match 88.5%; Score 269; DB 5; Length 131;
 Best Local Similarity 84.7%; Pred. No. 1e-25; Indels 0; Gaps 0;
 Matches 50; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KVGSLARAGKVGQTPKVAKEKKKKTGRARRMQYNRRFVNVVPTFGKKKGNPNS 59
 Db 73 KVGSLARAGKVGQTPKVAKEKKKKTGRARRMQYNRRFVNVVPTFGKKKGNPNS 131

RESULT 8
 Q9VDH8 PRELIMINARY; PRT; 132 AA.
 AC Q9VDH8;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE CG15697 protein (RH08962p).
 GN CG15697.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutten G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miles G.L.G.,
 RA Abiri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Bencze P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkov D., Botchan M.R., Buck J., Brockstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,


```
RT  elegans." ;
RL  Nature 368:32-38(1994).
(2)
RP  SEQUENCE FROM N.A.
RC  STRAIN-BRISTOL N2.
RA  Geisel C., Stellyes L., Bradshaw H.;
RT  "The sequence of C. elegans cosmid C26F1." ;
RL  Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
(3)
RN  SEQUENCE FROM N.A.
RC  STRAIN-BRISTOL N2.
RA  Waterston R.;
RL  Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR  EMBL; U53148; AAB37076.1; -.
DR  HSSP; P02248; IUBI.
DR  InterPro; IPR000626; Ubiquitin.
DR  Pfam; PF00240; Ubiquitin; 1.
DR  SMART; SM00213; UBO; 1.
SQ  SEQUENCE 130 AA; 14033 MW; 50DC09AFB9P48532 CRC64;

Query Match
Best Local Similarity 74.7%; Score 227; DB 5; Length 130;
Matches 45; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 KHGSLRAGKVRGOTPKVAKOEKKKKTKGRAKRMQYNRRFVNVVPTFGKKGPNNNS 59
Db 72 KHGSLRAGKVAQTPKVDKDKKKKGRAPFRVGYTRVNVVAGSGPKKGPNNNS 130
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RESULT 11
ID 015351 PRELIMINARY; PRT; 230 AA.
AC 015351;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE SEB4B (Fragment).
GN SEB4B (HUMAN).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
(1)
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS.
RA Ruehlmann A., Gupta A., Terhorst C.;
RT "A novel murine RRM-type protein and its human homolog." ;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X75315; CA53064.1; -.
DR HSSP; P09651; IUPI.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; Trm; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 230 AA; 25220 MW; C747D6500608461 CRC64;

Query Match
Best Local Similarity 36.8%; Score 112; DB 4; Length 230;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 RRMQYNRRFVNVVPTFGKKG 54
Db 1 RRMQYNRRFVNVVPTFGKKG 21
```

```
RESULT 12
Q97ZH4
ID Q97ZH4 PRELIMINARY; PRT; 52 AA.
AC Q97ZH4;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
```

```
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE LSU ribosomal protein S30E (tps30E).
GN RPS30E OR SSO6817.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
(1)
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aways M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moers A., Erasmo G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2." ;
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AE006714; AAK41214.1; -.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 52 AA; 6046 MW; A9EB9D3E4E7E744E CRC64;

Query Match
Best Local Similarity 34.4%; Score 104.5; DB 17; Length 52;
Matches 21; Conservative 51.2%; Pred. No. 9.2e-06;
Matches 12; Mismatches 12; Indels 1; Gaps 1;

Qy 3 HGSLLRAGKVRGOTPKVAKOEKKKKTKGRAKRMQYNRRV 43
Db 4 HGSLLRAGKVRGOTPKVAKOEKKKKTKGRAKRMQYNRRV 43
```

```
RESULT 13
ID 0971W4 PRELIMINARY; PRT; 55 AA.
AC 0971W4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Putative 30S ribosomal protein S30.
GN SRS139.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
(1)
RN SEQUENCE FROM N.A.
RP STRAIN=JCM 10545 / 7;
RX PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankal A., Kosugi H., Hasegawa A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Maeuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7." ;
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000985; BAB66306.1; -.
KW Ribosomal protein; Hypothetical protein; Complete proteome.
SQ SEQUENCE 55 AA; 6365 MW; 5C9404787BA65826 CRC64;
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Query Match
Best Local Similarity 33.4%; Score 101.5; DB 17; Length 55;
Matches 20; Conservative 48.8%; Pred. No. 2.3e-05;
Matches 11; Mismatches 11; Indels 1; Gaps 1;

Qy 3 HGSLLRAGKVRGOTPKVAKOEKKKKTKGRAKRMQYNRRV 43
Db 4 HGSLLRAGKVRGOTPKVAKOEKKKKTKGRAKRMQYNRRV 43
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RESULT 14
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Search completed: December 3, 2002, 14:32:53
Job time : 32 secs

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ID Q8SR05      PRELIMINARY;      PRT;      59 AA.
AC Q8SR05;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 40S ribosomal protein S30.
GN ECU10_1575.
OS Encephalitozoon cuniculi.
OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissbach J., Vivares C.P.;
RA "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL; AL590449; CAD25878.1; -.
SQ SEQUENCE 59 AA; 6815 MW; C3A4A9AB33488FDB CRC64;

Query Match      31.2%; Score 95; DB 5; Length 59;
Best Local Similarity 45.9%; Pred. No. 0.00016;
Matches 17; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 5 SLARAGKVRGQTPKVAQEKKKKTKGRAKRRMQYNRR 41
DB 5 TINKAGKVRNQTDPDPVVEKERRKCGRCRQLKFEKR 41

RESULT 15
Q8ZV51      PRELIMINARY;      PRT;      55 AA.
ID Q8ZV51;
AC Q8ZV51;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Ribosomal protein S30.
GN PAE2455.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RA "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009877; AAL64205.1; -.
KW Complete proteome.
SQ SEQUENCE 55 AA; 6200 MW; E2F91102FE9EFF90 CRC64;

Query Match      28.8%; Score 87.5; DB 17; Length 55;
Best Local Similarity 48.7%; Pred. No. 0.0012;
Matches 19; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

QY 3 HGSLLARAGKVRGQTPKVAQEKKKKTKGRAKRRMQYNRR 41
DB 4 HGSLLTAKGKVRNQTPKI--PAKPRKNLTTPRRNIRNYKER 41
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 3, 2002, 14:30:49 / Search time 14 Seconds
(without alignments)
123.997 Million cell updates/sec

Title: US-09-424-815E-1
Perfect score: 304
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	20.7	370	1	US-08-415-818-12 Sequence 12, Appl
2	63	20.7	370	2	US-08-894-236-12 Sequence 12, Appl
3	63	20.7	370	5	PCT-US96-01444-12 Sequence 12, Appl
4	59.5	19.6	315	4	US-09-615-192A-378 Sequence 378, App
5	54.5	17.9	171	4	US-09-134-001C-5286 Sequence 5286, App
6	54	17.8	290	2	US-08-903-801-1 Sequence 1, Appl
7	54	17.8	290	4	US-09-295-055-1 Sequence 1, Appl
8	53.5	17.6	714	2	US-08-990-114-3 Sequence 36, Appl
9	53.5	17.6	714	4	US-09-241-333-3 Sequence 3, Appl
10	53.5	17.6	714	4	US-09-615-192A-389 Sequence 389, App
11	53	17.4	318	4	US-07-920-281C-3 Sequence 3, Appl
12	53	17.4	1253	4	US-08-466-277-3 Sequence 3, Appl
13	53	17.3	135	4	US-09-134-001C-3305 Sequence 3305, Ap
14	52.5	17.3	351	4	US-08-476-008-57 Sequence 57, Appl
15	52.5	17.3	351	4	US-08-333-485-57 Sequence 57, Appl
16	52.5	17.3	427	1	US-08-306-063-57 Sequence 57, Appl
17	52.5	17.3	427	1	US-08-833-374-8 Sequence 8, Appl
18	52.5	17.3	427	4	US-09-137-440-57 Sequence 57, Appl
19	52.5	17.3	427	6	US-09-039-780A-119 Patent No. 5310667
20	52.5	17.3	427	6	US-09-039-780A-119 Patent No. 5310667
21	52.5	17.3	427	6	US-09-039-780A-119 Patent No. 5310667
22	52	17.1	28	1	US-08-384-212-1 Sequence 1, Appl
23	52	17.1	28	2	US-08-739-819-1 Sequence 1, Appl
24	52	17.1	35	1	US-08-384-212-2 Sequence 2, Appl
25	52	17.1	35	2	US-08-739-819-2 Sequence 2, Appl
26	52	17.1	88	4	US-09-134-001C-2855 Sequence 2855, Ap
27	52	17.1	88	4	US-09-134-001C-2855 Sequence 2855, Ap

28	52	17.1	139	3	US-08-464-841A-2 Sequence 2, Appl
29	52	17.1	143	3	US-08-464-841A-4 Sequence 4, Appl
30	52	17.1	154	4	US-08-871-732A-1 Sequence 1, Appl
31	52	17.1	154	4	US-09-346-510B-1 Sequence 1, Appl
32	51.5	16.9	59	2	US-08-460-890A-60 Sequence 60, Appl
33	51.5	16.9	59	3	US-08-167-641C-60 Sequence 60, Appl
34	51.5	16.9	59	4	US-08-460-971A-60 Sequence 60, Appl
35	51.5	16.9	59	4	US-08-462-040-60 Sequence 60, Appl
36	51.5	16.9	472	2	US-08-216-894-10 Sequence 10, Appl
37	51.5	16.9	472	4	US-09-115-746-10 Sequence 10, Appl
38	51.5	16.9	801	4	US-09-104-070-2 Sequence 2, Appl
39	51.5	16.9	1202	1	US-08-425-061-22 Sequence 22, Appl
40	51.5	16.9	1202	2	US-08-825-886-22 Sequence 22, Appl
41	51.5	16.9	1363	2	US-08-425-061-23 Sequence 23, Appl
42	51.5	16.9	1363	2	US-08-825-886-23 Sequence 23, Appl
43	51.5	16.9	1852	1	US-08-425-061-24 Sequence 24, Appl
44	51.5	16.9	1852	2	US-08-825-886-24 Sequence 24, Appl
45	51.5	16.9	1863	1	US-08-425-061-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-415-818-12
Sequence 12, Application US/08415818
Patent No. 5621079
GENERAL INFORMATION:
APPLICANT: Cascieri, Margaret A.
APPLICANT: Linemeyer, David L.
APPLICANT: MacNeil, Douglas J.
APPLICANT: Shiao, Lin-Lin
APPLICANT: Strader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,818
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/383,746
FILING DATE: 03-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET INFORMATION: 19390
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3462
TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-415-818-12
Query Match 20.7%; Score 63; DB 1; Length 370;

Gaps **0 :**

PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 378
LENGTH: 315
TYPE: PRT
ORGANISM: EucaIyptus grandis
US-09-615-192A-378

Query Match 19.6%; Score 59.5; DB 4; Length 315;
Best Local Similarity 31.8%; Pred. No. 4.1;
Matches 21; Conservative 8; Mismatches 18; Indels 19; Gaps 3;

QY 5 SLARAGKVRGQTPKVAKOEKKKKTKGRARMOYRRFVN-----VPTF--GKKK 53
DB 37 SLVRAG-----VAKAIKNERTGTASLLRLHPHDFVAGCDASILLDPTPSFVGKTA 88

QY 54 GPNVNS 59
DB 89 APNNNS 94

RESULT 5
US-09-134-001C-5286
Sequence 5286, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5286
LENGTH: 171
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5286

Query Match 17.9%; Score 54.5; DB 4; Length 171;
Best Local Similarity 25.8%; Pred. No. 9.4;
Matches 17; Conservative 12; Mismatches 20; Indels 17; Gaps 2;

QY 6 LARAGK-----VRGQTPKVAKOEKKKKTKGRAR--RMQYRRFVNVPPT 48
DB 106 LVGAGSLKRLQQLERARYEVGSDYERMKRKLAKQKRRKREAOXKOTRRFMSLRN 165

QY 49 FGKKGK 54
DB 166 TSORCG 171

RESULT 6
US-08-903-801-1
Sequence 1, Application US/08903801
Patent No. 5932712
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Puri V
TITLE OF INVENTION: NEW ANEXIN BINDING PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,801
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0354 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSONO1
CLONE: 2272281
US-08-903-801-1

Query Match 17.8%; Score 54; DB 2; Length 290;
Best Local Similarity 26.3%; Pred. No. 19;
Matches 15; Conservative 10; Mismatches 10; Indels 22; Gaps 2;
QY 9 AGKVRGQTPKVA-----KOEKKKKTKGRARMOYRRFVNVPPTFGKKKGN 56
DB 208 ASEKAKETPAADDDNCGDKKKKKKKKKGEKEKEKE-----KKKGS 251

RESULT 7
US-09-295-055-1
Sequence 1, Application US/09295055
Patent No. 6232440
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Puri V
TITLE OF INVENTION: NEW ANEXIN BINDING PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/903,801
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749

APPLICATION NUMBER: 08/990,114
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0451 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 128842
US-09-241-333-3

Query Match 17.6%; Score 53.5; DB 4; Length 714;
Best Local Similarity 23.7%; Pred. No. 60;
Matches 18; Conservative 9; Mismatches 20; Indels 29; Gaps 1;

QY 6 LARAGVRCQTPKVA-----KOEKKKKTKGRAKRM 36
DB 4 LAKAGTHEAKMAHPKVEDESEDESEBDDSSGSEVVIPOKKGKATATPAKKY 63

QY 37 QYNRRFVNVPFPGKK 52
DB 64 VVSQTKKVAVPTPAKK 79

RESULT 11
US-09-615-192A-389
Sequence 389, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 389
LENGTH: 318
TYPE: PRT
ORGANISM: Pinus radiata
US-09-615-192A-389

Query Match 17.4%; Score 53; DB 4; Length 318;
Best Local Similarity 27.6%; Pred. No. 29;
Matches 21; Conservative 10; Mismatches 27; Indels 18; Gaps 3;

QY 2 VHGSLARA--GKVRGQTPKVAQ-----EKKKKTKGRAKRMQYNRRFV----- 43
DB 22 VNGQLSTFYAKSCPRLPISVVKQAVAKKMGASLVRLHFHDFVNGCDGSIILLDD 81

QY 44 NVVPTFGKKKGPVANS 59
DB 82 NATFTGKTKAGPNNANS 97

RESULT 12
US-07-920-281C-3
Sequence 3, Application US/07920281C
Patent No. 5739026
GENERAL INFORMATION:
APPLICANT: Garoff, Henrik
APPLICANT: Liljestrom, Peter
TITLE OF INVENTION: DNA Expression Systems Based on
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/920,281C
FILING DATE: 13-AUG-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 828-103P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-920-281C-3

Query Match 17.4%; Score 53; DB 1; Length 1253;
Best Local Similarity 44.0%; Pred. No. 13e+02;
Matches 11; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 10 GKVRGQTPKVAKOEKKKKTKGRAKR 34
DB 86 GKTQOQKKKDKQADKKKKPKGRER 110

RESULT 13
US-08-466-277-3
Sequence 3, Application US/08466277
Patent No. 6190666
GENERAL INFORMATION:
APPLICANT: Garoff, Henrik
APPLICANT: Liljestrom, Peter
TITLE OF INVENTION: DNA Expression Systems Based on
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2002, 14:31:22 / Search time 11 Seconds
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85.412 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 304
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Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	304	100.0	170	10	US-09-925-301-994
2	276	99.8	118	10	US-09-864-761-35333
3	62.5	20.6	206	10	US-09-214-881A-9
4	61	20.1	185	10	US-09-214-881A-7
5	60	19.7	86	10	US-09-864-761-31832
6	59	19.4	66	10	US-09-764-869-722
7	59	19.4	66	10	US-09-764-846-163
8	58	19.1	72	10	US-09-864-761-36199
9	58	19.1	208	10	US-09-214-881A-2
10	58	19.1	209	10	US-09-214-881A-6
11	58	19.1	209	10	US-09-214-881A-8
12	57	18.8	79	10	US-09-764-846-193
13	57	18.8	170	10	US-09-864-761-39624
14	56.5	18.6	54	10	US-09-864-761-45531
15	55.5	18.3	98	10	US-09-764-846-229
16	55.5	18.3	241	10	US-09-938-803-8
17	55.5	18.3	1043	10	US-09-946-805-4
18	55	18.1	533	10	US-09-431-226-5
19	55	18.1	747	10	US-09-431-226-7

20	54.5	17.9	63	10	US-09-764-846-185	Sequence 185, App
21	54.5	17.9	72	10	US-09-864-761-35548	Sequence 35548, A
22	54.5	17.9	76	10	US-09-764-869-960	Sequence 960, App
23	54.5	17.9	76	10	US-09-764-846-257	Sequence 257, App
24	54.5	17.9	86	10	US-09-864-761-46660	Sequence 46660, A
25	54.5	17.9	150	10	US-09-764-846-225	Sequence 225, App
26	54	17.8	71	10	US-09-864-761-37061	Sequence 37061, A
27	54	17.8	76	9	US-10-002-344A-229	Sequence 229, App
28	54	17.8	141	10	US-09-864-761-36181	Sequence 36181, A
29	54	17.8	290	10	US-09-808-885-1	Sequence 1, Appli
30	54	17.8	525	10	US-09-814-550-2	Sequence 2, Appli
31	53.5	17.6	61	10	US-09-764-846-261	Sequence 261, App
32	53.5	17.6	68	10	US-09-764-846-189	Sequence 189, App
33	53.5	17.6	83	10	US-09-864-761-34889	Sequence 34889, A
34	53.5	17.6	130	10	US-09-815-242-12016	Sequence 12016, A
35	53.5	17.6	130	10	US-09-815-242-13732	Sequence 13732, A
36	53.5	17.6	369	10	US-09-925-300-1070	Sequence 1070, Ap
37	53.5	17.6	498	10	US-09-764-864-1122	Sequence 1122, Ap
38	53.5	17.6	714	10	US-09-978-242-3	Sequence 3, Appli
39	53	17.4	57	10	US-09-864-761-41286	Sequence 41286, A
40	53	17.4	63	10	US-09-764-846-260	Sequence 260, App
41	53	17.4	1253	10	US-09-901-106-3	Sequence 3, Appli
42	52.5	17.3	45	10	US-09-764-846-258	Sequence 258, App
43	52.5	17.3	351	10	US-09-893-238-11	Sequence 11, Appl
44	52.5	17.3	427	9	US-09-464-099A-57	Sequence 57, Appl
45	52.5	17.3	427	10	US-09-861-696-57	Sequence 57, Appl

ALIGNMENTS

```
RESULT 1
US-09-925-301-994
; Sequence 994, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 994
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-994

Query Match      100.0%; Score 304; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.6e-25;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHSLARAGKVRGQTPKVAKKKKKTKGRARRRQVRRFVVVPTFGKKKGNANS 59
Db 112 KVHSLARAGKVRGQTPKVAKKKKKTKGRARRRQVRRFVVVPTFGKKKGNANS 170

RESULT 2
US-09-864-761-35333
; Sequence 35333, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
```

APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 35333
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC009704.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 19
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 18
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 81
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 30
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 12
OTHER INFORMATION: SWISSPROT HIT: P35544, EVALUAE 4.00e-23
OTHER INFORMATION: EST_HUMAN HIT: BF347807.1, EVALUAE 6.00e-47
US-09-864-761-35333

Query Match 90.8%; Score 276; DB 10; Length 118;
Best Local Similarity 88.9%; Pred. No. 4.9e-26;
Matches 56; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

Qy 1 KVHGSARAGVGTGTPKVAQKK- - - KKTGTRAKRMQYNRRFVNVPVTFGKKKGP 56
Db 56 KVHGSARAGVGTGTPKVAQKKKKKKTGATRRMQYNRRFVNVPVTFGKKKGP 115

Qy 57 ANS 59
Db 116 ANS 118
RESULT 3
US-09-214-881A-9
Sequence 9, Application US/09214881A
Patent No. US20020009749A1
GENERAL INFORMATION:
APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Uesugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Yoshida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 206
TYPE: PRT
ORGANISM: Gallus gallus
US-09-214-881A-9

Query Match 20.6%; Score 62.5; DB 10; Length 206;
Best Local Similarity 32.1%; Pred. No. 1.3;
Matches 17; Conservative 9; Mismatches 12; Indels 15; Gaps 2;
Qy 9 AGKVRGOTPKVAQKKKKTKGRAKRMQYNRRFVNVPVTFGKKKG- - - PNA 57
Db 52 SSKEKGFEEMAKGDKAR- - - - - YDREMKNYVPPKGEKKKKKDPNA 93

RESULT 4
US-09-214-881A-7
Sequence 7, Application US/09214881A
Patent No. US20020009749A1
GENERAL INFORMATION:
APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Uesugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuwa
APPLICANT: Yoshida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 185
TYPE: PRT
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: MOD RES
LOCATION: (39)
OTHER INFORMATION: Xaa = Glu or Arg
NAME/KEY: MOD RES
LOCATION: (149)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-214-881A-7

```

1  OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.3
2  OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.8
3  OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 13
4  OTHER INFORMATION: EXPRESSED IN B7474, SIGNAL = 6.5
5  OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 12
6  OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.3
7  OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 9.1
8  OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.1
9  US-09-864-761-33832
10 Query Match 19.7%; Score 60; DB 10; Length 86;
11 Best Local Similarity 38.2%; Pred. No. 1;
12 Matches 13; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
13
14 QY 8 RAGKVRGQTPKVAKOEKKKKKTGRAKRRMOYRR 41
15 | | | | | | | | | | | | | | | | | |
16 | | | | | | | | | | | | | | | | | |
17 Db 12 RGRRRRRRRKKKKKKKKKKKKKKKKRRRRRRR 45
18
19 RESULT 6
20 US-09-764-869-722
21 Sequence 722, Application US//09764869
22 Patent No. US20020061521A1
23 GENERAL INFORMATION:
24 APPLICANT: Rosen et al.
25 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
26 FILE REFERENCE: PC007
27 CURRENT APPLICATION NUMBER: US//09/764,869
28 CURRENT FILING DATE: 2001-01-17
29 Prior application data removed - refer to PALM or file wrapper
30 NUMBER OF SEQ ID NOS: 2442
31 SOFTWARE: PatentIn Ver. 2.0
32 SEQ ID NO 722
33 LENGTH: 66
34 TYPE: PRT
35 ORGANISM: Homo sapiens
36 FEATURE:
37 NAME/KEY: SITE
38 LOCATION: (4)
39 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
40 NAME/KEY: SITE
41 LOCATION: (56)
42 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
43 US-09-764-869-722
44
45 Query Match 19.4%; Score 59; DB 10; Length 66;
46 Best Local Similarity 34.9%; Pred. No. 1;
47 Matches 15; Conservative 8; Mismatches 12; Indels 8; Gaps 1;
48
49 QY 1 KVHGSLARAG-----KVRGQTPKVAKOEKKKKKTGRAKR 35
50 | | | | | | | | | | | | | | | | | |
51 | | | | | | | | | | | | | | | | | |
52 Db 20 RVRSRSRRAAMTFSKKKKKKKKKKKKKKKKKKKKKKKK 62
53
54 RESULT 7
55 US-09-764-846-163
56 Sequence 163, Application US//09764846
57 Patent No. US20020102638A1
58 GENERAL INFORMATION:
59 APPLICANT: Rosen et al.
60 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
61 FILE REFERENCE: PT212
62 CURRENT APPLICATION NUMBER: US//09/764,846
63 CURRENT FILING DATE: 2001-01-17
64 Prior application data removed - consult PALM or file wrapper
65 NUMBER OF SEQ ID NOS: 348
66 SOFTWARE: PatentIn Ver. 2.0
67 SEQ ID NO 163
68 LENGTH: 66
69 TYPE: PRT
70 ORGANISM: Homo sapiens
71 FEATURE:
72 NAME/KEY: SITE

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; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (56)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-846-163

Query Match          19.4%; Score 59; DB 10; Length 66;
Best Local Similarity 34.9%; Pred. No. 1;
Matches 15; Conservative 8; Mismatches 12; Indels 8; Gaps 1;

Qy 1 KVHGSARAG-----KVRGTPKVAQKQKKKKTKTKRKR 35
Db 20 RVRSSRSRAASMTFSKXXXXXXXKKKKKKKKKKKKKKKKKKKKR 62

RESULT 8
US-09-864-761-36199
; Sequence 36199, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36199
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: MAP TO AC010826.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2
US-09-864-761-36199

Query Match          19.1%; Score 58; DB 10; Length 72;
Best Local Similarity 41.5%; Pred. No. 1.5;
Matches 17; Conservative 6; Mismatches 12; Indels 6; Gaps 2;

Qy 4 GSLARAGKVRGTPKVAQKQKKKKTKTKRKRMOYNNR 41
Db 24 GKRKRGKRR---RKVRKKEKKKTKRGRGRRRRRRR 61

RESULT 9
US-09-214-881A-2
; Sequence 2, Application US/09214881A
; Patent No. US20020009749A1
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-881A-2

Query Match          19.1%; Score 58; DB 10; Length 208;
Best Local Similarity 34.9%; Pred. No. 4.6;
Matches 15; Conservative 7; Mismatches 17; Indels 4; Gaps 1;

Qy 19 VAKQEKKKKTKGRKRMOYNNRFRNVVPTFGKKKG----PNA 57
Db 51 MSAKEKSKFEDMAKSDKARYDREMKNYVPPKGDKKKKKDPNA 93

RESULT 10
US-09-214-881A-6
; Sequence 6, Application US/09214881A
; Patent No. US20020009749A1
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
```



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      CURRENT APPLICATION NUMBER: US/09/214,881A
      CURRENT FILING DATE: 1999-06-07
      NUMBER OF SEQ ID NOS: 13
      SOFTWARE: PatentIn Ver. 2.1
      SEQ ID NO 6
      LENGTH: 209
      TYPE: PRT
      ORGANISM: Sus scrofa
US-09-214-881A-6

Query Match          19.1%; Score 58; DB 10; Length 209;
Best Local Similarity 34.9%; Pred.No. 4.6;
Matches 15; Conservative 7; Mismatches 17; Indels 4; Gaps 1

OY   19 VAKDEKKKKTGRARRMQYNRRFVNVVPTFGKKG----PNA 57
       :|::|||:         :|::|||:|||||
Db    51 MSAAEKSKFEDMAKS DKARYDREMKNYVPKGDKKGKKDPVA 93

RESULT 11
US-09-214-881A-8
Sequence 8, Application US/09214881A
Patent No. US20020009749A1
GENERAL INFORMATION:
APPLICANT: Ozaki, Shoichi
APPLICANT: Sobajima, Junko
APPLICANT: Uesugi, Hiroko
APPLICANT: Okazaki, Takahiro
APPLICANT: Tanaka, Masao
APPLICANT: Nakao, Kazuo
APPLICANT: Yoshida, Michiteru
APPLICANT: Shirakawa, Hitoshi
APPLICANT: Osakada, Fumio
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
FILE REFERENCE: 068383.0104
CURRENT APPLICATION NUMBER: US/09/214,881A
CURRENT FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 209
TYPE: PRT
ORGANISM: Rattus rattus
US-09-214-881A-8

Query Match          19.1%; Score 58; DB 10; Length 209;
Best Local Similarity 34.9%; Pred.No. 4.6;
Matches 15; Conservative 7; Mismatches 17; Indels 4; Gaps 1

OY   19 VAKDEKKKKTGRARRMQYNRRFVNVVPTFGKKG----PNA 57
       :|::|||:         :|::|||:|||||
Db    51 MSAAEKSKFEDMAKS DKARYDREMKNYVPKGDKKGKKDPVA 93

RESULT 12
US-09-764-946-193
Sequence 193, Application US/09764846
Patent No. US20020102638A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT12
CURRENT APPLICATION NUMBER: US/09/764,846
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 348
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 193
LENGTH: 79
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
```

[illegible]

